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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein August 30, 2004, 17:00:32 ; Search time 38 Seconds (without alignments) 192.383 Million cell updates/sec Run on:

07330446.PEP 405 1 gpdainapvtccynftnrki.....qkwvqdsmdhldkgtgtpkt Title: Perfect score: Sequence:

94

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	monocyte chemoattr	monocyte chemoattr	monocyte chemoattr	monocyte chemoattr		monocyte chemotact		eotaxin precursor	monocyte chemotact		PDGF-inducible JE	immediate-early se	monocyte chemoattr	eotaxin precursor	eotaxin precursor	monocytic cytokine	LD78-beta protein		macrophage inflamm			macrophage inflamm	macrophage inflamm	monocyte chemoattr	lymphocyte and mon	monocyte chemoattr	I-309 protein prec	lymphotactin precu	monocyte adherence
SUMMERTES								•				,																		
n o	ID	A60299	JC2136	A39296	0233	മ	A55984	54	JC4912	JC5295	JC2417	A30209	S07723	I48147	I48099	JC2478	A48093	B35673	A30574	A31767	I46730	C30552	I52322	A32393	A46539	JE0177	A28815	A37236	ETHUL	C60407
	DB	7	7	Н	7	7	7	N	~	N	Ŋ	٦	н	N	Ŋ	N	7	7	N	٦	N	N	N	7	Н,	~	Н	~	Н	N
	Length	66	66	9	99	125	72	109	97	66	66	148	148	120	96	96	97	93	92	92	92	92	92	92	91	120	91	96	114	20
ď	Query				77.8		71.1	70.9		66.2			59.5	58.3	52.8	51.1	49.4		35.2			31.5	30.4	29.4	26.8	26.2	26.0	٠.	24.6	24.2
	Score	405	337	315	315	314	288	287	270	268	261	252	241	236	214	207	200	145.5	142.5	135.5	133.5	127.5	123	119	108.5	106	105.5	99.5	99.5	86
	Result No.	-	01	m	4	Ω.	9	. 7	σ	Ø	10	11	12	13															28	29

interleukin-8 prec	ltws protein - mou lymphotactin precu	Neutrophil attract	interleukin-8 prec	interleukin-8 - ra	interleukin-8 - do	gene C10 protein -	, interleukin-8 prec	. cellobiose-phospho	hypothetical prote	F54F2.8 protein -	hypothetical prote	hypothetical prote		hypothetical prote
A53096	S24236 ETMSL	I48148	842496	146871	JN0841	149555	A37034	AG3481	876162	844825	T26700	E90097	F96831	AB2020
0.0	7 11	0	N	~	7	7	C)	N	7	N	7	0	~	7
103	114	101	101	101	95	116	9	2867	143	282	363	1019	1076	853
23.2	23.1	20.5	19.5	19.5	18.5	18.1	17.3	16.3	16.2	16.0	15.9	15.8	15.8	15.4
94	9 9 1 5 7	83	79	79	75	73.5	70	99	65.5	65	64.5	64	64	62.5
30	32	33	34	35	36	37	38	39	40	41	42	43	44	4 .

ALIGNMENTS

A60299	
monocyte chemoattractant protein 1 precursor - human	
N;Alternate names: GDCF-1; glioma-derived monocyte chemotactic factor 1; MCAF;	AF;
N;Contains: glioma-derived chemotactic factor 2 (GDCF-2)	

RESULT 1

MCP-1; mor

C)Date: 20-Feb-1993 #sequence revision 20-Feb-1993 #text change 16-Jul-1999 C;Accession: A35474; A33476; S03339; IS1841; A60299; A32300; A32396; A34561; IS7488; JC1(R;Shyy, Y.J.; Li, Y.S.; Kolattukudy, P.E. Asiochem. Biophys. Res. Commun. 169, 346-351, (1990) A A;Title: Structure of human monocyte chemotachic protein gene and its regulation by TPA. A;Reference number: A35474; MUID:90290466; PMID:2357211

A; Molecule type: DNA
A; Residues: 1-99 < CSH7.
A; Residues: 1-99 < CSH7.
A; Cross-references: GB: M7719; NID: 9187447; PIDN: AAA18102.1; PID: 9487124
B; Rollins, B.J.; Stier, P.; Ernst, P. Mong, G.G.
Mol. Cell. Biol. 9, 4687-469; F1989
A; Tille: The human homolog of the Figure encodes a monocyte secretory protein.
A; Reference number: A33476; MUID: 90097880; PMID: 2513477
A; Accession: A33476
A; Molecule type: MRNA
A; Residues: 1-99 < ROL>

A;Cross-references: GB:N30816; GB:N31625; GB:N31626; NID:g188701; PIDN:AAA36330.1; PID:gr. S;Yoshimura, T.;Yuhki, N.; Moore, S.K.; Appella, B.; Lerman, M.I.; Leonard, B.J.; PEBS Lett. 244, 487-493, 1989 FEBS Lett. 244, 487-493 (1989) A;Title: Human monocyte chamaetractant protein-1 (MCP-1). Full-length cDNA cloning, exp

A,Reference number: S03339, MUID:89153605, PMID:2465924
A,Accession: S03339
A,Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-99 < YOS>
A;Cross-references: GB:X14768; NID:934513; PIDN:CAA32876.1; PID:934514
A;Experimental source: glio...
A;Experimental source: glio...
Adv. Exp. Med. Biol. 305, 47-56 (1991)
A;Fiteference number: I51841; MUID:92095166; PMID:1661560
A;Accession: I51841

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-99 <YVO2>
A;Across-references: GB:S71513; NID:g240867; PIDN:AAB20651.1; PID:g240868
R;Bottazzi, B.; Colotta, F.;Sica, A.; Nobili, N.; Mantovani, A.
Int. J. Cancer 45, 795-797, (1990)
A;Title: A chemoattractant expressed in human sarcoma cells (tumor-derived chemotactic f

A;Reference number: A60299; MUID:90216082; PMID:2182547 A;Accession: A60299

A,Status: not compared with conceptual translation A,Molecule type: mRNA

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Page

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A;Title: Porcine luteal cells express monocyte chemoattractant protein-1 (MCP-1): Analysi A;Reference number: JC2136; MUID:94183284; PMID:7510962
A;Accession: JC2136
A;Accession: JC2136
A;Accession: JC2136
A;Residues: 1-99 <HOS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           monocyte chemoattractant protein 1 precursor - bovine
NyAlternate names: monocyte chemotactic factor 1; seminal plasma protein P6
C;Species: Bos primiganius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A39296; B39296
C;Accession: A39296; B39296; MUDD:92096117; PMID:1721821
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A;Residues: 1-99 - vWEM>
A;Cross-references: GB:M84602; GB:M85264; NID:g163394; PIDN:AAA30651.1; PID:g163395
A;Accession: B39296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;24-99/Product: monocyte chemoattractant protein-1 #status predicted <MAT>
F;94/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 QPDAINSPUTCCYTLTSKKISMQRLMSYRRVTSSKCPKBAVIFKTIAGKBICABBYQKWV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Cross-references: EMBL:X79416; NID:9872312; PIDN:CAA55945.1; PID:9872313
                                                                                                                                                                A; Cross-references: GB: Z48479; NID: g683716; PIDN: CAA88370.1; PID: g683717
R; Zach, O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

83.2%; Score 337; DB 2; Length 99;
Best Local Similarity 80.0%; Pred. No. 1.6e-31;
Matches 60; Conservative 8; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 77.8%; Score 315; DB 1; Length 99; Local Similarity 73.3%; Pred. No. 5.3e-29; Pred. S5; Conservative 13; Mismatches 7; Indels
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F;1-23/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Keywords: glycoprotein
F;1-23/Domain: signal sequence #status predicted
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A, Residues: 50-68, x', 70-74, x', 76 <WE2>
A, Experimental source: seminal vesicle.
C, Superfamily: macrophage inflammatory protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C, Superfamily: macrophage inflammatory protein
                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, July 1994
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                                                                                                                                                                                                                                                                                                                 A; Reference number: S57497
                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-99 <ZAC>
                                                                                                                                                                                                                                                                                                                                                A, Accession: S57498
A, Status: preliminary
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           A; Residues: 1-99 < EDOT>

A; Residues: 1-99 < EDOT>

B; Furutani, Y:; Nomura, H:; Notake, M:; Oyamada, Y.; Fukui, T.; Yamada, M.; Larsen, C.G. B; Diochem.

Biochem. Biophys. Res. Commun. 159, 249-255, 1989

A; Fitle: Cloning and sequencing of the cDNA for human monocyte chemotactic and activatinn A; Reference number: A32300; MUID:89165862; PMID:2923622

A; Accession: A32300

A; Residues: not compared with conceptual translation

A; Molecule type: mRNA

A; Residues: 1-99 < FURA

A; Residues: A32396; MUID:89184525; PMID:2648385

A; Residues: YX, 25-99 < ROB>

A; Molecule type: protein

A; Molecule type: protein

A; Molecule type: protein

A; Residues: YX, 25-99 < ROB>

B; Conings, R:; Lenaerts, J; Billiau, A:; Van Damme, J.

B; Decock, B:; Conings, R:; Lenaerts, J; D90;

A; Fitle: Identification of the monocyte chemocatic protein from human osteosarcoma cell

A; Reference number: A34561; MUID:90211336; PMID:2322286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: A34561
A;Molecule type: protein
A;Residues: 29-33,'XX',36-52,82-92 <DEC>
R;Li, Y.S.; Shyy, Y.J.; Wright, J.G.; Valente, A.J.; Cornhill, J.F.; Kolattukudy, P.E.
R»D. Cell. Blochem: 126, 61-68, 1993
A;Title: The expression of monocyte chemotactic protein (MCP-1) in human vascular endoth
A;Reference number: 157488; MUID:94150478; PMID:8107690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Map position: 17q11,2-17q12
(S,Superfamily; macrophage inflammatory protein
(S,Superfamily; macrophage inflammation; pyroglutamic acid
(S,CyVords: Cytokine; glycoprotein, inflammation; pyroglutamic acid
(S,CyVords: Cytokine; glycoprotein, inflammation; pyroglutamic acid
(S,1-23/Domain: signal sequence #status predicted <SIG>
(S,2-9-9)/Product: monocyte chemoattractant protein 1 #status experimental <MAT>
(S,2-9-9)/Product: monocyte chemoattractant protein 1, short form #status experimental <MAT>
(S,2-4)/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment (S,37/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A,Status: translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Rosidues: 1-99 < LIX>
A,Cross.references: GB:S69738; NID:g545464; PIDN:AAB29926.1; PID:g545465
B,Ye, Q.N.; Su, G.F.; Yuan, Y.; Huang, C.F.
Chinese J, Microbiol. Immunol. 14, 29-32, 1994
A,Title: The PCR, cloning and sequencing of human monocyte chemoattractant protein-1
A,Reference number: JC1096
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 16-Jul-1999
C;Accession: JC2136; S57498
R;Hosang, K.; Knoke, I.; Klaudiny, J.; Wempe, F.; Wuttke, W.; Scheit, K.H.
Biochem. Biophys. Res. Commun. 199, 962-968, 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Accession: JC1096
A;Molecule type: mRNA
A;Residues: 24-28,'Q',30-99 <YEQ>
C;Genetics:
A;Gene: GDB:SCYA2
A;Cross-references: GDB:125279; OMIM:158105
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Matches 76; Conservative
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Gaps

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9 83

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Gaps

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9

C; Superfamily: macrophage inflammatory protein

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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 16-Jul-1999
C;Accession: A54678; JC1478; S32222
R;Opdenakker, G; Fiten, P.; Nys, G.; Froyen, G.; Van Roy, N.; Speleman, F.; Laureys, G.
Rsoponakker, J. 403-408, 1994
A;Title: The human MCP-3 gene (SCYA7): cloning, sequence analysis, and assignment to the A;Reference number: A54678; MUID:94375065; PMID:7916328
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: GDE-X72309
R;Opdenakker, G.; Froyen, G.; Fiten, P.; Proost, P.; Van Damme, J.
A;Cross-references: Gommun. 191, 535-542, 1993
A;Title: Human moncoyte chemotactic protein. 3 (MCP-3): Molecular cloning of the CDNA and A;Reference number: JC1478; MUID:93213290; PMID:8461011
A;Accession: JC1478
A;Accession: JC1478
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R;Minty, A.; Chalon, P.; Guillemot, J.C.; Kaghad, M.; Liauzun, P.; Magazin, M.; Miloux, submitted to the EMBL Data Library, March 1993
A;Description: Molecular cloning of MCP-3: a human monocyte-derived monocyte chemoattrac A;Reference number: S32222
A;Accession: S32222
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C;Comment: This protein induces proteinase secretion and chemotaxis by macrophages and C;Genetics:
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                                                                                                                                                                                                                                                                                1 DAINSPVICCYTLTSKKISMQRLMSYRRVTSSKCPKBAVIFKTIAGKEIXAEP--KWVQD
                                                                                                                                                                                                                                      3 DAINAPVICCYNFINRKISVQRLASYRRIISSKCPKEAVIFKIIVAKBICADPKQKWVQD
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A;Cross-references: GDB:138473; OMIM:158106
A;Cross-references: GDB:138473; OMIM:158106
A;Introns: 36/1; 75/2
C;Superfamily: macrophage inflammatory protein
C;Reywords: cytckine; glycoprotein; inflammation
F;1-33/Domain: signal sequence #staus predicted <SIG>F;34-109/Product: monocyte chemotactic protein 3 #status predicted
F;34-Binding site: carbohydrate (Asn) (covalent) #status predicted
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Pred. No. 9.6e-26;
4; Mismatches 17; Indels
                                                                                 Length 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N;Alternate names: monocyte chemoattractant protein MCP-3
                                          ; DB 2; Lem.
.4.9e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    monocyte chemotactic protein 3 precursor - human
                                                                        y Match 71.1%; Score 288; DE Local Similarity 74.0%; Pred. No. 4.9e hes 54; Conservative 8; Mismatches
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1 Similarity 72.0%; Pre
54; Conservative 4;
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                                                                                                                                                                                                                                                                                                                                                                                                    63 SMDHLDKOTOTPK 75
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Best Local Similarity
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A; Residues: 1-109 <0P2>
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A; Residues: 1-109 <MIN>
                                                                                     Query Match
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Gpecies: Oryctolagus cuniculus (domestic rabbit)
C;Gpecies: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 16-Jul-1999
C;Accession: 146857
J; Tmmunol. 146, 3483-3488, 1991
A;Fitle: Neutrophil attractant/activation protein-1 and monocyte chemoattractant protein A;Reference number: 146857, MUD:91225489; PMID:2026877
A;Accession: 146857
A;Accession: 146857
A;Residues: 1-125 < YOS>
A;Csoperfamily: macrophage inflammatory protein
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C;Species: Bos primigenius taurus (cattle)
C;Daccies: Dos primigenius taurus (cattle)
C;Daccesion: A55884
R;Procst, P.; Wuyts, A.; Lenaerts, J.P.; Van Damme, J.
Biochemistry 33, 13406-13412, 1994
A;Title: Purification, sequence analysis, and biological characterization of a second by Accession: A55884
A;Reference number: A55984
A;Referen
monocyte chemoattractant protein-1 - bovine
C;Species: Bos prinigenius indicus (zebu cattle)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 03-May-1996
C;Accession: UC2336
B;Wempe, F:; Kuhlmann, U.K.; Scheit, K.H.
B;Wempe, F:; Kuhlmann, U.K.; Scheit, K.H.
A;Title: Characterization of the bovine monocyte chemoattractant protein-i gene.
A;Reference number: UC2336; MUID:94338337; PMID:8060303
A;Accession: UC2336
A;Molecule type: protein
A;Residues: 1:99 cMEM>
C;Genetics:
A;Gene: MCP-1
A;Introns: 26/1; 65/2
C;Superfamily: macrophage inflammatory protein
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Best Local Similarity 73.3%; Pred. No. 5.3e-29;
Matches 55; Conservative 13; Mismatches 7; Indels
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Best Local Similarity 75.0%; Pred. No. 8.8e-29;
Matches 57; Conservative 10; Mismatches 9;
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QDAIANLDKKMQTPKT 99
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ODSINYLNKKNOTPK 98
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Matches
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C; Accession: JC2417
R; Hosang, K.; Knoke, I.; Klaudiny, J.; Wempe, F.; Wuttke, W.; Scheit, K.H.
R; Hosang, K.; Knoke, I.; Klaudiny, J.; Wempe, F.; Wuttke, W.; Scheit, K.H.
B; Hosang, K.; Knoke, I.; Klaudiny, J.; Wempe, F.; Wuttke, W.; Scheit, K.H.
B; Hosang, K.; Knoke, I.; Kes. Commun. 205, 148-153, 1994
A; Reference number: JC2417; MUD:95091716, PMID:7999015
A; Accession: JC2417
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: I-99 < HOS.
A; Kross-references: GB:248480; NID:9683718; PIDN:CAA88371.1; PID:9683719
A; Experimental source: Corpus luteum
C; Superfamily: macrophage inflammatory protein
F;1-23/Domain: signal sequence #status predicted <NAT>
F;24-99/Product: monocyte chemoattractant protein-2 #status predicted <NAT>
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DGF-inducible JE glycoprotein precursor - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A30209; A44771; A30861
R;Rollins: B.U.; Morrison, E.D.; Stiles, C.D.
Proc. Natl. Acad. Sci. U.S.A. 85, 3738-3742, 1988
A;Title: Cloning and expression of JE, a gene inducible by platelet-derived growth factor.
A;Reference number: A30209; MUID:88234501; PMID:3287374
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A;Cross-references: GB:M19681; NID:g193486; PIDN:AAA37684.1; PID:g387168; GB:M19682
R;Kawahara, R.S.; Deuel, T.F.
B;Kawahara, R.S.; Deuel, T.F.
J. Biol. Chem. 264, 679-682, 1989
A;Title: Platelet-derived growth factor-inducible gene JE is a member of a family of A;Reference number: A44771; MUID:89093129; PMID:2910858
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               24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 16-Jul-1999
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C.Genetics:
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C;Keywords: cytokine; glycoprotein
F;126/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A; Residues: 1-148 < KA2>
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A; Molecule type: DNA
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eotaxin precursor - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 20-Jun-2000
C;Accession: 074912
R;Bartels, J; Schlueter, C; Richter, E; Noso, N; Kulke, R; Christophers, E; Schroe Biochem. Biophyrs. Res Commun. 225, 1045-1051, 1996
A;Title: Human dermal fibroblasts sociaxin: Molecular cloning, mRNA expression, A;Reference number: JC4912; MUID:96374440; PMID:8780731
A;Reference number: JC4912; MUID:96374440; PMID:8780731
A;Retus: preliminary
A;Molecule type: mRNA
A;Residues: 1-97 cBARS
A;Crossion: JC4912
A;Stetus: preliminary
A;Residues: 1-97 cBARS
A;Crossion: Gérmal fibroblast
C;Comment: This protein has eosinophil specific chemotatic activity.
C;Comment: This protein has eosinophil specific chemotatic activity.
C;Comment: fibroblast
C;Reywords: fibroblast
F;1-18/Domain: signal sequence #status predicted cMAT>
F;19-97/Froduct: eotaxin #status predicted cMAT>
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Pred. No. 7.6e-24;
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C,Species: Sus scrofa domestica (domestic pig)
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Query Match Best Local Similarity

Matches

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Best Local Similarity Matches 47; Conserv

Query Match

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C;Species trust norvegicus (Norway rat)
C;Date: 21-Fab-1995 #sequence_revision 05-Apr-1995 #text_change 16-Jul-1999
C;Accession: JC2478
R;Jose, P.J; Adocek, I.M.; Griffiths-Johnson, D.A.; Berkman, N.; Wells, T.N.C.; William Biochem. Biophys. Res. Commun. 205, 788-794, 1994
A;Title: Botaxin: Cloning of an eosinophil chemoattractant cytokine and increased mRNA e A;Reference number: JC2478; WUID:95091818; PMID:7999113 52.8%; Score 214; DB 2; ilarity 57.4%; Pred. No. 2e-17; Conservative 12; Mismatches 17 Search completed: August 30, 2004, 17:08:02 Job time : 40 secs 68 DKQTQTPK 75 88 GQISQTTK 95 88 DQISQTTK 95 68 рКОТОТРК 75 Query Match Best Local Similarity Matches 39; Conserv eotaxin precursor - rat q ઠે ð a ò В ઠ N;Alternate names: monocyte chemoattractant protein-1
C;Species: Rattus norvegious (Norway rat)
C;Species: Rattus norvegious (Norway rat)
C;Date: 10.58p-1999 #sequence_revision 10-5ep-1999 #text_change 10-5ep-1999
C;Accession: 807723; JN0128
R;Timmers, H.T.M; Pronk, G.J.; Bos, J.L.; van der Eb, A.J.
Nucleic Acids Res 18, 22-34, 1990
A;Title: Analysis of the rat JE gene promoter identifies an AP-1 binding site essential
A;Reference number: 807723; MUID:90174947; PMID:2106664
A;Residues: 1-148 arINA
A;Cross-references: RBEL:X17053; MID:955530; PIDN:CAA34901.1; PID:955531
A;Residues: 1-148 arINA
A;Cross-references: RBEL:X17053; MID:91285530; PIDN:CAA34901.1; PID:955531
A;Residues: T.; Takeya, M.; Takabashi, K.
Biochem: Blobhys: Res. Commun. 174, 504-509, 1991
A;Title: Molecular cloning of rat monocyte chemoattractant protein-1 (MCP-1) and its exp
A;Residues: 1-148 arX05.
A;Residues: 1-148 product: immediate-early serum-responsive protein JE #status predicted cMAT>
F;24-148/Product: immediate-early serum-responsive protein JE #status predicted cMAT> CyAccession: 148147

R;Yoshiumra, T.

J. Immunol. 150, 5025-5032, 1993

A;Title: cDNA cloning of guinea pig monocyte chemoattractant protein-1 and expression of A;Reference number: 148147, MUID:93267104; PMID:8496603

A;Accession: 148147

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Nolecule type: mRNA
A;Residues: 1-120 eRES>
A;Cross_references: GB:L04985; NID:9349820; PIDN:AAA37047.1; PID:9349821 7 ö 9 81 1 QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV 60 24 QPDAVNAPLTCCYSFTGKMIPMSRLENYKRITSSRCPKEAVVFVTKLKREICADPNKEWV 83 monocyte chemoattractant protein-1 - guinea pig
C,Species: Cavia porcellus (guinea pig)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999 24 QPDGVNTP-TCCYTF-NKQIPLKRVKGYERITSSRCPQEAVIFRTLKNKEVCADFTQKWV 1 OPDAINAPVICCYNFINRKISVORLASYRRIISSKCPKBAVIFKTIVAKEICADPKOKWV Gaps 7 ő Ouery Match 59.5%; Score 241; DB 1; Length 148; Best Local Similarity 55.3%; Pred. No. 2.4e-20; Matches 42; Conservative 16; Mismatches 18; Indels Length 120; Query Match 58.3%; Score 236; DB 2; Length 12 Best Local Similarity 59.7%; Pred. No. 7.4e-20; Matches 43; Conservative 14; Mismatches 13; Indels C; Superfamily: macrophage inflammatory protein 61 QDSMDHLDKQTQTPKT 76 OKYIRKLDONOVRSET 99 61 QDSMDHLDKQTQ 72 ODYIAKLDORTO 93 82 84 ò В ò 8,8 qq

cisecies: Cavia porcellus (guinea pig)
Cispecies: Oz-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 16-Jul-1999
Ciscosion: 148099
M.E.; Luster, A.D.; Lilly, C.M.; Drazen, J.M.; Leder, P.
J. Exp. Med. 181, 1211-1216, 1995
A.Title: Constitutive and allergen-induced expression of ectaxin mRNA in the guinea pig
A.Reference number: 148099; MUID:95173589; PMID:7869037
A.Accession: 148099
A.Accession: 148099
A.Residuary; translated from GB/EMBL/DDBJ
A.Residuars: preliminary;
A.Molecule type: mRNA
A.Residuars: 1-96 cRES.
A.Residuars: 1-96 cRES.
A.Residuars: 1-96 cRES.
A.Residuary and Coppage inflammatory protein ô 8 PVICCYNFINRKISVQRLASYRRITSSKCPKEAVIFKTIVAKBICADPKQKWVQDSMDHL 67 28 PSACCFRVINKKISFQRLKSYKIIISSKCPQTAIVFEIKPDKMICADPKKKWVQDAKKYL 87 Gaps 0 Length 96; 17; Indels

A,Molecule type: mRNA A,Residues: 1-96 <10S> A,Cross-references: EMBL:X77603; NID:g602551; PIDN:CAA54698.1; PID:g602552 C:Comment: This protein is identified as a potent eosinophil chemoattractant. C;Superfamily: macrophage inflammatory protein

Gaps . Query Match 51.1%; Score 207; DB 2; Length 96; Best Local Similarity 55.9%; Pred. No. 1.3e-16; Matches 38; Conservative 12; Mismatches 18; Indels

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QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV 60
                                           QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKBAVIFKTIVAKEICADPKQKWV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: VISIONIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER: ED201-4714
COMPUTER: ED201-4714
COMPUTER: ED201-4714
COMPUTER: ED201-4714
COMPUTER: ED201-4714
COMPUTER: ED201-4714
COMPUTER: ED201-4716
COM
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ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: WILLIAMS, TIMOTHY J.
APPLICANT: JOSE, PETER J.
APPLICANT: GRIFFITHS-JOHNSON, DAVID A.
APPLICANT: HSUAN, JOHN J.
TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/08615232A
Patent No. 5993814
                                                                                                                                                             QDSMDHLDKQTQTPKT 76
                                                                                                                                                                                                                                       61 ООЅМОНГОКОТОТРКТ 76
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 amino acids
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: WILLIA
                                                                                                                                                                                                                                                                                                                                                                                                              US-08-615-232A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-615-232A-5
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RESULT 3 CUS-08-470-323-5

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1 OPDAINAPVTCCYNFTNRKISVORLASYRRITSSKCPKEAVIFKTIVAKEICADFKOKWV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 405; DB 4; Length 76; Best Local Similarity 100.0%; Pred. No. 6.1e-47; Matches 76; Conservative 0; Mismatches 0; Indels
                 PERMETAL INFORMATION US/US4/U323A

GENERAL INFORMATION:
APPLICANT: WILLIAMS, TMOTHY J.
APPLICANT: GENETRA,
APPLICANT: GENETITHS-JOHNSON, DAVID A.
APPLICANT: GENETITHS-JOHNSON, DAVID A.
APPLICANT: GENETITHS-JOHNSON, DAVID A.
APPLICANT: GENETITHS-JOHNSON, DAVID A.
APPLICANT: HISUN, JOHN J.
TILE REFERENCE: 550-33
CURRENT APPLICATION NUMBER: US/08/470,323A
CURRENT FILING DATE: 1993-06-14
EARLIER APPLICATION NUMBER: PT/GB94/02006
FEARLIER FILING DATE: 1993-09-14
EARLIER FILING DATE: 1994-04-29
NUMBER: OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: WILLIAMS, TIMOTHY J.
APPLICANT: JOSE, PETER J.
APPLICANT: GRIFFITHS-OOHNSON, DAVID A.
APPLICANT: HSUAN, JOHN J.
TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
FILE REPERENCE: 550-33
CURRENT APPLICATION NUMBER: US/9/195,457
CURRENT FILING DATE: 1998-11-18
PRIOR PILING DATE: 1998-0-06
PRIOR FILING DATE: 1995-0-06
PRIOR FILING DATE: 1994-09-14
PRIOR PILING DATE: 1994-04-29
NUMBER: OF SEQ ID NOS: 11
SEQ ID NO S: LINGUELLY TO
Sequence 5, Application US/08470323A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09195457; Patent No. 6605702; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 QDSMDHLDKQTQTPKT 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: human
US-08-470-323-5
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US-09-195-457-5
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61 ODSMDHLDKOTOTPKT 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-330-163-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floran:

MEDIUM TYPE: Floran:

COPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patenth Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/291,038

FLILING DATE: 14-Apr-1999

CLASSIFTCATION AD47:

RELING DATE: 13-A0G-1996

APPLICATION NUMBER: GB 9318984

FILING DATE: 13-A0G-1996

APPLICATION NUMBER: GB 9408602

FILING DATE: 29-APR-1994

ATTORNEY/AGENT INPORMATION:

NAME: WITEGO AND AND ATTORNEY AND ATTORNEY/AGENT INPORMATION:

NAME: WITEGO AND AND ATTORNEY AND ATTORNEY/AGENT INPORMATION:

NAME: WITEGO AND AND ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 405; DB 4;
Best Local Similarity 100.0%; Pred. No. 6.1e-47;
Matches 76; Conservative 0; Mismatches 0;
                                                                                                                                                                                  Sequence 5, Application US/09291038
Patent No. 6635251
GENERAL INPORMATION:
APPLICANT: WILLIAMS, TIMOTHY J.
JOSE, PETER J.
GRIFFITHS-JOHNSON, DAVID A.
HSUAN, JOHN J.
TITLE OF INVENTION: CHEMOTACTIC CYTOKINE
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REPERENCE/DOCKET NUMBER: 550-32
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEPAX: (703) 816-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-291-038-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/08330163
Patent No. 5656724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 76 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
  61 ODSMDHLDKQTQTPKT 76
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US-08-330-163-12
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US-09-291-038-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV
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Sequence 12, Application US/08482111

APPLICANT: Daly, Thomas J.
APPLICANT: Daly, Thomas J.
APPLICANT: LaRosa, Gregory J.
TITLE OF INVENTION: Chemokine-Like Proteins and Methods of J. (UNMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
APPLICANT: Daly, Thomas J.
APPLICANT: LaRosa, Gregory J.
TITLE OF INVENTION: Chemokine-Like Proteins and Methods of TITLE OF INVENTION: Use
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 405; DB 1; Length 78; Best Local Similarity 100.0%; Pred. No. 6.3e-47; Matches 76; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            STATE: MA

COUNTRY: U.S.A.

ZIP: 0210-2804

ZIP: 0210-2804

COMPUTER: FOLOPY disk
MDDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,163
FILING DATE: US-05-MG-1994
CLASSIFICATION STORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 32,983
REFERENCE/DOCKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: MA
COUNTRY: U.S.A.
ZIP. 202110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
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1 QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV 60
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APPLICANT: SHARMA, Lawrence Rajendra
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTONREY/AGBRT INPORMATION:
NAME: BRIXT, Stephen A
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 405; DB 1;
Pred. No. 6.3e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 405; D
Best Local Similarity 100.0%; Pred. No. 6.3
Matches 76; Conservative 0; Mismatches
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                                                                                                                                                             00231/083001
             UMBER: US/08/482,111
07-JUN-1995
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US-08-127-499A-35
US-08-127-499A-35
Sequence 35, Application US/08127499A
Patent No. 5510264
GENERAL INFORMATION
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fease, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/POCKET NUMBER: 00231
REFERENCE/POCKET NUMBER: 00231
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-8906
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 51
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 904136
INFORMATION FOR SEQ ID NO: 35:
SEGUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 QDSMDHLDKQTQTPKT 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 орѕмонгокототект 78
                                                                                                                                                                                                                                                                                          LENGTH: 78 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LECURAL: (2021)
TELEPHONE: (2021)
TELEPHONE: (2021)
                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
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USA
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US-08-127-499A-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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TITLE OF INVENTION: PEPPIDES REPRESENTING EPITOPIC SITES FOR TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
                                                                                      1 OPDAINAPVICCYNFINRKISVORLASYRRIISSKCPKEAVIFKTIVAKEICADPKOKWV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKBAVIFKTIVAKEICADPKQKWV 83
                                                                                                                    24 QPDAINAPVICCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPRQKWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 OPDAINAPVTCCYNFTNRKISVORLASYRRITSSKCPKEAVIFKTIVAKEICADPKOKWV
                                              Gaps
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                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
CLASS!FICATION NUMBER: US 08/127,499
FILING DATE: 28-SED-1993
ATTORNEY/AGBNT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/POCKET NUMBER: 51916/104/INBI
Query Match
Best Local Similarity 100.0%; Pred. No. 8.6e-47;
Matches 76; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

Best Local Similarity 100.0%; Pred. No. 8.6e-47;
Matches 76; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 3000 K Street, N.W., Suite 500 CITY: Washington STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                      NG-08-482-847-35
Sequence 35, Application US/08482847
Sequence 35, Sef757
Patent No. 5556757
PATENT INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
                                                                                                                                                                               61 QDSMDHLDKQTQTPKT 76
                                                                                                                                                                                                                         84 ÓDSMDHLDKÓTÓTPKT 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 99 aminor
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(202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown US-08-482-847-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS:
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24 QPDAINAPVICCYNFINRKISVQRLASYRRIISSKCPKBAVIFKTIVAKEICADPKQKWV 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 405; DB 1; Length 99; Best Local Similarity 100.0%; Pred. No. 8.6e-47; Matches 76; Conservative 0; Mismatches 0; Indels
3: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                           STREET: 6300 Sears Tower, 233 South Wacker Drive CITY: Chicago STATE: Illinois CUMTAY: United States of America ZIP: 60606-6402 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/480,449
                                                                                                                                                                                                                                                                                                                                                                                                                      PPLICATION TO THE STATE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) NAME/KEY: misc feature
) OTHER INFORMATION: "Hu MCP-1"
US-08-480-449-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 QDSMDHLDKQTQTPKT 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
US-08-480-49-19
Sequence 19, Application US/08480449
Fatent No. 568827
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
APPLICANT: Gray, Patrick W.
TILLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE
NUMBER OF SEQUENCES: 24
                                                                                                    GENERAL INFORMATION:
APPLICANT: Wilde, Craig G.
APPLICANT: Hawkins, Phillip R.
APPLICANT: Bandman, Olga
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: EXPRESSED CHEMOKINES, THEIR
TITLE OF INVENTION: PRODUCTION AND USES
NUMBER. OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER PRADMBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRACESQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/347,492B
FILING DATE: 29-NOV-1994
PRIOR APPLICATION NUMBER: 08/320,011
FILING DATE: 05-OCT-1994
APPLICATION NUMBER: 08/320,011
FILING DATE: 05-OCT-1994
APPLICATION NUMBER: 33,954
ATTORNER: Litther, Barbara J
RECISTRATION NUMBER: 33,954
REFERENCE/DOCKET NUMBER: 33,954
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELEFAX: 415-852-0555
INFORMATION FOR SEQ ID NO: S
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
                                      Sequence 8, Application US/08347492B Patent No. 5602008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 QDSMDHLDKQTQTPKT 76
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MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: GI 487124
US-08-347-492B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: siz
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US-08-479-126B-5

| Sequence 5, Application US/08479126B
| Patent No. 5866373
| Patent No. 5866373
| APPLICANT: LI, HADDONG
| APPLICANT: RIJEN, STEVEN M
| APPLICANT: SUTTON, GRANGER G III
| TITLE OF INVENTION: POLYNUCLECTIDES ENCODING HUMAN MONOCYTE
| TITLE OF INVENTION: CHEMOTACTIC PROTEIN-4 (AS AMENDED)
| NUMBER OF SEQUENCES:
| CORRESPONDENCE ADDRESS:
| ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
| STREET: 1100 NEW YORK AVENUE, SUITE 600
| CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: DC
COUNTRY: USA
ZIP: 2005-3934
ZIP: 2005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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1 QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV 60
                                                                                                                                                                                                                                                                                                 24 QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV 83
                                                                                                                                                     Length 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08726830A

Patent No. 5880263

GENERAL INFORMATION:
APPLICANT: LI HADDONG
APPLICANT: SUTTON, GRANGER G III
APPLICANT: SUTTON, MONOCYTE CHEMOTACTIC PROTEIN-4
ITITLE OF INVENTION: MONOCYTE CHEMOTACTIC PROTEIN-4
NUMBER OF SEQUENCES 6
CORRESPONDENCE ADDRESS:
ADDRESSE: STEAME, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                      Indels
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COMPUTER: 1EM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/726,830A
FILING DATE: US-OCT-1996
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Best Local Similarity 100.0%; Pred. No. 8.6e-47;
Matches 76; Conservative 0; Mismatches 0;
                                                                                                                                                     Query Match
100.0%; Score 405; DB 2;
Best Local Similarity 100.0%; Pred. No. 8.6e-47;
Matches 76; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: STEFFE, ERIC K
REGISTRATION UNDBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0340002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 08-OCT-1996
CLASIFICATION: 435
PRIOR PEDLICATION 0475
APPLICATION NUMBER: 08/479,126
FILING DATE: 07-JUN-1995
REOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,425
FILING DATE: 21-APR-1995
RICR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05384
APTICATION NUMBER: PCT/US94/05384
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    61 QDSMDHLDKQTQTPKT 76
                                                                                                                                                                                                                                                                                                                                                                                                      84 QDSMDHLDKQTQTPKT 99
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          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                        ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-421-144A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20005-3934
COMPUTER READABLE FORM:
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTI
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US-08-726-830A-5
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APPLICANT: BANDMAN, OLGA
APPLICANT: COLEMAN, ROGER
APPLICANT: COLEMAN ROGER
TITLE OF INVENTION: NEW CHEMOKINE EXPRESSED IN BOSINOPHILS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
CARRESPEES: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 100.0%; Score 405; DB 2; Length 99; Best Local Similarity 100.0%; Pred. No. 8.6e-47; Matches 76; Conservative 0; Mismatches 0; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/421,144A
FILING DATE: 13-APR-1995
CLASSIFICATION: 435
ATTONENY/AGENT INPOMMATION:
NAME: Luther, Barbara J.
REGISTRATION NUMBER: 33954
RESPERENCE/DOCKET NUMBER: PF-0031 US
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET UNDER: 1488.0340001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
INFORMATION FOR SEG ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 99 amino acids
APPLICATION NUMBER: US/08/479,126B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,425
FILING DATE: 21-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05384
FILING DATE: 16-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAMB: STEFFE, BRIC K
REGISTRATION NUMBER: 36,689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 31/4 CTTY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-479-126B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-08-421-144A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
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                                                                                                                                                                                                                                                                      PREFILE OF INVENTION:
GOMERAL INFORMATION:
GOMERAL INFORMATION:
GOMERAL INFORMATION:
APPLICANT: GOAGISKA, ROCARD
APPLICANT: GOAGISKA, ROCARD
TITLE OF INVENTION: MACROPHAGE DERIVED CHEMOKINE AND CHEMOKINE
TITLE OF INVENTION: ANALOGS
NUMBER OF SEQUENCES: 32
CORRESPONDERS: MATCHALL, O'TOOLE, GERSEIN, MALTAY & BOTUN
STREET: 6300 SCATS TOWEY, 233 SOUTH WACKET DIIVE
COUNTRY: United States of America
STATE: 111Anole States of America
COUNTRY: United States of America
ZIP: 66606-642
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Datantin Release #1.0, Version #1.30
COMPUTER: Datantin Release #1.0, Version #1.30
COMPUTER: Datantin Release #1.0,
COMPUTER: Datantin Release
SOFTWARE: Datantin Release
COMPUTER: Datantin STATE
COMPUTER: Datantin Release
SOFTWARE: Datantin Release
APPLICATION NUMBER: 08/79,620
FILING DATE: 18-00V-1995
ATTORNEY/ASTIN NUMBER: 27866/33318
FREFERENCE/DOCKET INFORMATION:
TELEDHOME: 312/474-630
TELEDHOME: 312/474-630
TELEDHOME: 312/474-634

TELECOMMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 Amino acid
STRANDEDBESS: shingle
TYPE: AMINORALIES SHINGLES
FRANDEDBESS: shingle
TOOLOGY: LINER
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 8.6e-47;
Matches 76; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                   RESULT 15
US-08-660-542-19
; Sequence 19, Application US/08660542
; Patent No. 5912703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: misc_feature
OTHER_INFORMATION: "Hu MCP-1"
FEATURE:
                                                                                                                             84 QDSMDHLDKQTQTPKT 99
                                                                                         61 ODSMDHLDKOTOTPKT 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Protein
; LOCATION: 1..76
US-08-660-542-19
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61 QDSMDHLDKQTQTPKT 76

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84 QDSMDHLDKQTQTPKT 99

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Search completed: August 30, 2004, 17:08:40 Job time : 35 secs

Wed Sep

(oldsu) Andla ego9 sint

1 08:47:04 2004 Wed Sep GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

sw model protein search, using OM protein August 30, 2004, 16:51:56; Search time 122 Seconds (without alignments) 176.013 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

07330446.PEP 405 1 qpdainapvtccynftnrki.....qkwvqdsmdhldkqtqipkt Scoring table:

76

1586107 segs, 282547505 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A Geneseq 29Jan04:*

1: geneseq11980s:*

2: geneseq12000s:*

4: geneseq12001s:*

5: geneseq12001s:*

7: geneseq12003as:*

7: geneseq12003as:*

8: geneseq12003as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Aar28660 MCF. 3/20	Monocy (0 Amino	Human	Aao14143 Human MCP	Aam53048 Human mon	Adc89673 Human mat	Add14998 Human mon		Ade06777 Human MCP	7 Ниша	~	Aar73914 Human mon	Aar70800 Chemoattr	4	Monoc	Aay48391 Human pro	Human	4	Aam52440 HIV_Nef1	9 Human	1060	Abp65214 Hypoxia-r	5799 Human	Abul0502 Human MCP
SOLUMINA SOL	ΙΩ	AAR28660	AAR87680	AAY69030	AA020010	AA014143	AAM53048	ADC89673	ADD14998	ADE80852	ADE06777	AAP95387	AAR28663	AAR73914	AAR70800	AAW40174	AAY26176	AAY48391	AAB15785	AAB97914	AAM52440	AAU77179	ABB80901	ABP65214	ABP96799	ABU10502
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	Length	76	16	76	76	76	76	16	76	76	16	66	66	66	9	66	ov Ov	a o	ov ov	O)	თ თ	9	o o	66	9	66
dю	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0		100.0	100.0		100.0	100.0	100.0
	Score	405	405	405	405	405	405	405	405	405	405	405	405	405	405	405	405	405	405	405	405	405	405	405	0	0
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	Ade48100 Human mon	Add14997 Human mon	Aay69049 A chemoki	Aay69050 A chemoki		. Aaw40175 Macrophag			Aar06398 Human MCF	Aap90292 Peptide f	Aaw09374 Monocyte	Aaw11131 Mature hu	Aar86859 Mature MC	9	Aar87677 (3-Ala) M	Aar87675 (28-Asp)	Aay14222 Chemokine	Aar53398 Sense MCP	Adc89672 Human MCP
ADC89670	ADE48100	ADD14997	AAY69049	AAY69050	AAY69051	AAW40175	AAB12818	ADC89671	AAR06398	AAP90292	AAW09374	AAW11131	AAR86859	AAR87676	AAR87677	AAR87675	AAY14222	AAR53398	ADC89672
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66	o o	122	325	327	3	76	76	77	66	16	16	76	77	16	76	76	77	16	77
100.0	100.0	100.0	100.0	100.0	100.0	99.3	99.3	0.66	0.66	98.8		8.8		ω,	98.0	97.5	96.5	9	0.96
405	405	405	405	405	405	402	402	401	401	400	400	400	400	397	397	395	391	389	389
26			50	30	31	32	33	3.4	32	36	3.7	38	9.6	40	4	42	43	44	4.5

ALIGNMENTS

RESULT 1 AAR28660

AAR28660 standard; protein; 76 AA.

AAR28660;

(revised)
(first entry) 25-MAR-2003 24-MAR-1993

MCF.

Plasmid, monocyte chemotactic factor; MCF; translation; termination; terminator; initiation; ribosome binding site; RBS; promoter; tryptophan; repressor

Synthetic.

W09219737-A1

12-NOV-1992.

92WO-JP000550. 27-APR-1992;

91JP-00135950. 09-MAY-1991; Yamagishi J, Matsuo N, Fukui T,

(DAIN) DAINIPPON PHARM CO LTD.

Yamada M;

WPI; 1992-398864/48. N-PSDB; AAQ30745, AAQ30746.

Prodn. of polypeptide(s) having monocyte-chemotactic activity - using expression plasmids with E. coli elements and specific E.coli strains

Claim 1; Page 48 + Page 36; 56pp; English.

An expression plasmid, pHM483, for producing MCF(76) consisting of 76 amino acids was constructed. The prod. can be used for e.g. treating bacterial infectious diseases. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 76 AA;

Gaps .; 0 Query Match 100.0%; Score 405; DB 2; Length 76; Best Local Similarity 100.0%; Pred. No. 8.7e-43; Matches 76; Conservative 0; Mismatches 0; Indels

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0/330446.pep.rag

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The present sequence represents a chemokine receptor ligand. The present ligand can be incorporated into the conjugates of the invention. The specification describes a conjugate, computaing a targeted agent and a chemokine receptor ligand. The conjugate binds to a chemokine receptor resulting in internalisation of the targeted agent in cells bearing the receptor. The conjugates are used for formulating a medicament or for treating disorders associated with inflammatory responses resulting from activation, proliferation and migration of immune effector cells. The disorders or disease states comprise secondary tissue damage such as central nervous system (CNS) injury, CNS inflammatory diseases, neurodegenerative disorders, heart disease, inflammatory edgeseses, inflammatory bind diseases, inflammatory has thyroiditis, or cytokine-
     immune effector cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chemokine; anti-HIV; antiasthmatic; antiarthritic; antirheumatic; antiarteriosclerotic; dermatological; antiinflammatory; antiallergic;
Chemokine receptor; ligand; inflammatory response; immune effector cesecondary tissue damage; central nervous system injury; MCP-1; CNS inflammatory disease; neurodegenerative disorder; heart disease; inflammatory bowel disease; inflammatory bowel disease; inflammatory joint disease; inflammatory kidney; renal disease; inflammatory lung disease; inflammatory nasal disease; inflammatory thyroid disease; thyroiditis; cytokine-regulated cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QPDAINAPUTCCYNFINRKISVQRLASYRRIISSKCPKEAVIFKTIVAKEICADPKQKWV
                                                                                                                                                                                                                                                                                                                                                                                                                     A new therapeutic agent comprising a conjugate for treating secondary tissue damage and other disease conditions like Alzheimer's disease, stroke, Parkinson's disease and atherosclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 405; DB 3;
100.0%; Pred. No. 8.7e-43;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 60; 204pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human chemokine MCP-1 protein.
                                                                                                                                                                                                                                                99WO-CA000659.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ODSMDHLDKOTOTPKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 QDSMDHLDKQTQTPKT
                                                                                                                                                                                                                                                                                                                                                     Coggins PJ;
                                                                                                                                                                                                                                                                                                                  (OSPR-) OSPREY PHARM LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                   Mcdonald JR,
                                                                                                                                             domo sapiens
                                                                                                                                                                                                                                                21-JUL-1999;
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AAO20010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   comprising a growth factor, comprises a monocyte chemotactic activating factor (MCAE) or its variants or derivatives. The factor has potent effect on skin wounds and ulcers. The present sequence is human MCAE, the activity of which is exemplified as the new remedy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a new remedy for curing wounds which, instead of
   9
                    QPDAINAPVICCYNFINRKISVQRLASYRRITSSKCPKBAVIPKTIVAKEICADPKQKWV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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 QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QPDAINAPVICCYNFINRKISVQRLASYRRIISSKCPKEAVIFKTIVAKEICADPKQKWV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                              Monocyte chemotactic activating factor for use as wound remedy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wound treatment using monocyte chemotactic factor - has potent therapeutic effect on skin wounds and ulcers.
                                                                                                                                                                                                                                                                                                                               monocyte chemotactic activating factor; MCAF; wound remedy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 405; DB 2;
100.0%; Pred. No. 8.7e-43;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 12; 22pp; Japanese.
                                                                                                                                                                                         AAR87680 standard; protein; 76 AA.
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                                                                                                   61 obsmphipkororpkr 76
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                                                                   QDSMDHLDKQTQTPKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Naruto M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TORA ) TORAY IND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-131181/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 76 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                   WO9507710-A1
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                                                                   61
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ID AAX6
XX AAX6
XC AAX6
XX DT 30-b
XX XX
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WPI; 2002-083059/11.
N-PSDB; ABA02497.
           (GRYP-) GRYPHON SCI
                                                   WPI; 2002-171703/22
                                                                                               terminus analogs.
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                                                                                                                                                                                                                                     Sequence 76 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Egashira K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM53048;
                               Offord R,
                                                                                                                                                                                                                                                                                                                                                                                                             AAM53048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, chemokine receptor modulator; chemokine; HIV infection; AIDS; asthma; allergic rhinitis; atopic dermatitis; atheroma; antimilammatory; antiasthematic; antiallergic, dermatological; antiarteriosclerotic; antirthritic; anti-HIV; immunosuppressive; MCP-1; atherosclerosis; organ transplant rejection; rheumatoid arthritis.
                                                                                                                                                                                                                                                                   The invention relates to polymer-modified bioactive synthetic chemokines and to methods for their production and use. The compounds and methods of the backbone of the invention are useful in the analysis and treatment of various diseases states e.g. HIV and AIDS related disorders, asthma, allergic rhinitis, atopic dermatitis, atheroma/atherosclerosis, organ transplant rejection, and rheumatoid arthritis. This sequence represents the human chemokine MCP-1 protein of the invention
immunosuppressive; polymer-modified bioactive synthetic chemokine; HIV; AIDS; asthma; allergic rhinitis; atopic dermatitis; rheumatoid arthritis; atheroma; atherosclerosis; organ transplant rejection; MCP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                      1 OPDAINAPVICCYNFINRKISVORLASYRRIISSKCPKEAVIFKTIVAKEICADPKOKWV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QPDAINAFVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV 60
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                 New polymer-modified bioactive synthetic chemokines useful in the treatment of various diseases or disorders e.g. asthma.
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                                                                                                                                                                                                                                                                                                                                                                            Length 76;
                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                      Chen S,
                                                                                                                                                                                                                                                                                                                                                                            Score 405; DB 5;
Pred. No. 8.7e-43;
; Mismatches 0;
                                                                                                                                                                      Bradburne JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAO14143 standard; protein; 76 AA.
                                                                                                                                                                                                                                                Claim 8; Fig 10A; 176pp; English
                                                                                                                                                                                                                                                                                                                                                                             100.0%; Sc
100.0%; Pr
cive 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76
                                                                                                         12-JUL-2001; 2001WO-US021933
                                                                                                                              12-JUL-2000; 2000US-0217683P
                                                                                                                                                                        p,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QDSMDHLDKQTQTPKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QDSMDHLDKQTQTPKT
                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human MCP-1 protein.
                                                                                                                                                                                             WPI; 2002-268857/31.
                                                                                                                                                   (GRYP-) GRYPHON SCI
                                                                                                                                                                        Kochendoerfer G,
                                                                WO200204015-A1.
                                                                                                                                                                                                                                                                                                                                                          Sequence 76 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200204499-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-APR-2002
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                                                                                     17-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA014143;
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                                             Ношо
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AAO14143
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                                                                                                                                                                                                                                                                                     The present invention relates to chemokine receptor modulators, which comprise a chemokine polypeptide chain modified at N-terminus with an alliphatic chain and at least one amino acid derivatives and/or modified at its C-terminus with an alliphatic chain or polycyclic. The modulators can be used to treat diseases such as HIV infection, AIDS, asthma, allergic rhinitis, atopic dermatitis, atheroma, atherosclerosis, organ transplant rejection and rheumatoid arthritis. The present sequence is the human MCP-1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, monocyte chemoattractant protein-1, MCP-1, C-C chemokine family; pulmonary hypertension; primary; hypotensive.
                                                                                                              Chemokine receptor modulator useful for treating e.g. asthma, allergic rhinitis comprises a chemically modified carboxyl-terminus and/or amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 OPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QPDAINAFVTCCYNFTNRKISVQRLASYRRITSSKCFKEAVIFKTIVAKEICADFKQKWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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/note= "These residues are deleted in a specifically
claimed human MCP-1 mutent, 7ND-MCP-1 (AAM53049)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 405; DB 5;
100.0%; Pred. No. 8.7e-43;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM53048 standard; protein; 76 AA.
   Hartley O;
                                                                                                                                                                                                                                         Example 3; Fig 2; 86pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 ODSMDHLDKQTQTPKT 76
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(EGAS/) EGASHIRA K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100...
Best Active
76; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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Gaertner H,
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hypertension, comprising an antagonistic inhibitory mutant of monocyte chemoattractant protein-1 (MCP-1), DNA encoding the mutant MCP-1, or a neutralising antibody against MCP-1. MCP-1 is a member of the C-C chemokine family. The preventives and remedies have hypotensive activity and can be used in the prevention and treatment of pulmonary hypertension particularly pulmonary primary hypertension. The present sequence represents wild-type human MCP-1
Preventives and remedies for pulmonary hypertension containing mutant of MCP-1 antagonistic inhibitory type or its salt, encoded DNA or
                                                                                                                                                The invention relates to preventives and remedies for pulmonary
                                                                                           Disclosure; Page 31; 39pp; Japanese.
                       MCP-1 antagonistic inhil neutralization antibody
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Sequence 76 AA;

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QPDAINAPVICCYNFINRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV 60
                                                         1 QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADFKQKWV 60
                               Gaps
                               .
 Length 76;
                              0; Indels
100.0%; Score 405; DB 5;
100.0%; Pred. No. 8.7e-43;
iive 0; Mismatches 0;
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                            76; Conservative
               Local Similarity
 Query Match
                              Matches
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ADC89673 standard; protein; 76 AA 01-JAN-2004 ADC89673; ADC89673 RESULT TID STANKE STANK S

(first entry)

Human mature MCP-1 SEQ ID NO:4.

human; MCP-1; monocyte chemoattractant protein; MCP; immunosuppressive; antiinifalmmatory; cytostatic; antimicrobial; vasotropic; gene therapy; MCP-2; MCP-4; MCP-4; Ectaxin; leukocyte migration; leukocyte activation; vascular disorder; cancer; inflammatory; autoimmune disease; infection.

Synthetic

Homo sapiens.

WO2003084993-A1,

16-OCT-2003

10-APR-2002; 2002US-0371442P

09-APR-2003; 2003WO-EP050097

(ISTF) ARS APPLIED RES SYSTEMS HOLDING NV

Kosco-Vilbois M,

Proudfoot A,

Handel T;

WPI; 2003-804294/75.

New antagonists of MCP proteins, useful in preparing a composition for treating or preventing diseases related to excessive leukocyte migration and activation e.g. vascular, inflammatory or autoimmune disease, cancer or infection. Example 3; SEQ ID NO 4; 63pp; English.

The invention relates to novel antagonists of MCP proteins comprising mutants of MCP proteins in which the following combinations of residues, numbered on the sequence of human mature MCP-1, are substituted to Alanine, Glycine, Serine, Threonine, Proline, Aspartic Acid, Asparagine,

of a medical device implanted within a portion of a living body comprising contacting a portion of the living body in contact with the device with a monocyte chemoattractant protein 1 (MCP-1) antagonist to inhibit chronic inflammation induced by the presence of the medical device or fibrous encapsulation of the medical device. The method is useful for enhancing the biocompatibility of a medical device implanted in a portion of a living body by inhibiting chronic inflammation or

The invention describes a method of enhancing (MI) the biocompatibility

Disclosure; SEQ ID NO 3; 18pp; English.

antagonist.

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Glutamic Acid or Glutamine: 18 and 19; 18 and/or 19, together with 58; 18 and/or 19, together with 66; 18 and/or 19, together with 66; 18 and/or 19, together with 66; and 18 and/or 19, together with 66; and 66; and in a vacine with 66; and 67. A protein of the invention has immunosuppressive, antiinflammatory, cytostatic, antimicrobial, and vasotropic activity. The protein may have a use in gene therapy, and in a vaccine. The MCP proteins are human MCP-1, human MCP-2, human MCP-3, human MCP-4 or human Botaxin. The MCP antegonists are useful in preparing a composition for treating or preventing diseases distance to excessive leukocyte migration and activation, e.g., vascular disorders, cancer, inflammatory or autoimmune disease or infection. The present sequence is used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enhancing biocompatibility of a medical device implanted in a portion of a living body by contacting the portion of the body that is in contact with the implanted device with monocyte chemoattractant protein 1 (MCP-1)
                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                            1 QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV 60
                                                                                                                                                                                                                                                                                                                    1 QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiinflammatory; MCP-1 Antagonist; biocompatibility; medical device; monocyte chemoattractant protein 1; MCP-1; MCP-1 antagonist; chronic inflammation; fibrous encapsulation; human.
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human monocyte chemoattractant protein-1 (MCP-1) mature protein.
                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                  Length 76;
                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                Query Match
100.0%; Score 405; DB 7;
Best Local Similarity 100.0%; Pred. No. 8.7e-43;
Matches 76; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                           61 ODSMDHLDKOTOTPKT
                                                                                                                                                                                                                                                                                                                                                                                                                      61 ODSMDHLDKQTQTPKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-787133/74.
N-PSDB; ADD14996.
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                                                                                                                                                                                                                Sequence 76 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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ADE06777;
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                                                       RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a nuclear targeting peptide (ADE80826) comprising a nuclear targeting domain isolated from the C-terminal sequence of the ESkine and PESKY cheenchines. The nuclear targeting domain allows the protein to translocate to the cell nucleus. The nuclear targeting peptide is useful in preparing a medicament for treating cancer, particularly Burkitt's lymphoma or nasopharyngeal carcinoma. The present sequence is a chemokine sequence, used in a sequence alignment in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for treating
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                                                                                                                    1 QPDAINAPVTCCYNFINRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
  formation of fibrous capsules around the device. This is the amino acid sequence of human monocyte chemoattractant protein-1 (MCP-1) mature
                                                                                                        1 QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKOKWV
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                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nuclear targeting peptide comprising a nuclear targeting domain isolated from a chemokine, useful for preparing a medicament for tre cancer, particularly Burkitt's lymphoma or nasopharyngeal carcinoma.
                                                                                                                                                                                                                                                                                                          Nuclear targeting peptide; nuclear targeting domain; ESkine; PESKY; chemokine; cancer; cytostatic; huMCP1; chemokine.
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                                                               Length 76;
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                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                             Score 405; DB 7;
Pred. No. 8.7e-43;
; Mismatches 0;
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100.0%; Pred. No. 8.7e-43;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                        ADE80852 standard; peptide; 76 AA.
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                                                             100.0%; Sc
100.0%; Pr
cive 0;
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Query Match
Best Local Similarity 100...
Best 76; Conservative
                                                                                                                                                                  ODSMDHLDKQTQTPKT
                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                61 QDSMDHLDKQTQTPKT
                                                                                    Conservative
of fibrous
                                                  Query Match
Best Local Similarity
76; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-788341/74.
                                                                                                                                                                                                                                                                                      huMCP1 chemokine.
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                                          Sequence 76 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 76 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the invention
                                                                                                                                                                                                                                                                  29-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Graham G;
                                                                                                                                                                                                                                            ADE80852;
                       protein.
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The invention relates to a novel monocyte chemoattractant protein-1 (MCP-cardiant nucleic acid. A protein of the invention has immunosuppressive, cardiant, neuroprotective, antimicrobial, and cytostatic activity. A polymucleotide of the invention may have a use in gene therapy. The protein, nucleic acid, composition and method are useful for diagnosing or treating a MCP-1 mutein-related condition, e.g. immune, cardiavascular, neurologic or infectious or malignant disorders. The present sequence represents human MCP-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New monocyte chemoattractant protein-1 (MCP-1) mutein nucleic acid, useful for diagnosing or treating a MCP-1 mutein-related condition, e.g. immune, cardiovascular, neurologic or infectious or malignant disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 OPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV
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                                                                                                                                                                                                                                                                                                                                                                                                human; MCP-1; monocyte chemoattractant protein-1; immunosuppressive; cardiant; neuroprotective; antimicrobial; cytostatic; gene therapy; immune disorder; cardiovascular disorder; neurological disorder; infectious disorder; malignant disorder.
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100.0%; Pred. No. 8.7e-43;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 1; 81pp; English.
                                                                                                                                                       ADE06777 standard; protein; 76 AA.
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61 ODSMDHLDKOTOTPKT
                                                                                                                                                                                                                                                                            (first entry)
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Les 76; Conservative
                                                                                                                                                                                                                                                                                                                                      Human MCP-1 SEQ ID NO:1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003083059-A2.
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(revised)
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N-PSDB; AAQ30748.
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                                                                                                                                                                                                                                                                                                                                                                      /amagishi J,
                                                                                                                                                                                                                                                                         27-APR-1992;
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05-DEC-1995
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                                                repressor.
                                                                             Synthetic
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                                                                                                                                                             Protein
                                                                                                                             Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is a human-derived monoyte chemo-attractant peptide (MCP-1) sequence mol. mass of c.a. 8,400 D. MCP-1 can be used for treating infection eg inflammatory disease, or for the control of neoplasms by accumulation of monocytes at the site of the infection. The corresp. DNA is obtd. by chemical synthesis, by screening reverse trascripts of mRNA from purified blood leukcytes or cell cultures of eg U-373 MG or KMG-E. (Note: Revised entry submitted to correct the patent number format of US Government-numbers. For further information please with negoing US granted patent numbers. For further information please visit the Derwent web site at www.derwent.com/dwpi/updates/ntis_us.html.) (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human derived monocyte chemo:attractant peptide prods. - obtd. from human glioma cell line U-105MG or peripheral blood mono:nuclear leukocytes.
                                                                             Human monocyte chemo-attractant peptide; inflammatory disease; neoplasms.
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100.0%; Pred. No. 1.2e-42;
ive 0; Mismatches 0;
                                                Human monocyte chemo-attractant peptide-1.
                                                                                                                                                                                                                                                                                                                                         (USSH ) US DEPT HEALTH & HUMAN SERVICE.
(USDC ) US SEC OF COMMERCE.
(USDC ) US SEC OF COMMERCE.
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                                                                                                                                              Location/Qualifiers
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/product= "MCP-1"
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 (revised)
(first entry)
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                                                                                                               Homo sapiens
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 17-DEC-2001
25-JUL-1989
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(revised)
(first entry)

25-MAR-2003 24-MAR-1993

MCF.

AAR28663;

AAR28663 ID AAR2 XX AAR2 AC AAR2 XX DT 25-W DT 24-W XX DE MCF.

RESULT 12

Matches

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Plasmid, monocyte chemotactic factor; MCF; translation; termination; terminator; initiation; ribosome binding site; RBS; promoter; tryptophan;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Prodn. of polypeptide(s) having monocyte chemotactic activity - using expression plasmids with E. coli elements and specific E.coli strains.
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Best Local Similarity 100.0%; Pred. No. 1.2e-42;
Matches 76; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human monocyte chemoattractant factor hMCP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Fukui T, Yamada M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 43-44; 56pp; English.
                                                                                                                                        1. .23
/label= sig_peptide
24. .99
/label= mat_protein
                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                          92WO-JP000550.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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Gaps

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83

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Screening for cpds. with anti-heparanase activity - by detecting inhibition of heparin or heparan sulphate degradation, potentially useful for treating arthritis, restenosis, cancer.
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infection; human; monocyte receptor; chemotactic response; inflammation;
monocyte infiltration.
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                                                                                                                                                                                              Purified heparanases, prepared under reducing conditions and activated with transglutaminase, are given in AAR70786-804. Most are prepared by reverse transcription of mRNA from activated human leukocytes, then cloning of the cDNA into pVL1392 bacultovirus vector, and expression in Sf9 cells in the presence of reduced glutathione and dithiothreitol. (Updated on 25-MAR-2003 to correct PN field.)
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37. .39
/note= "potential N-linked glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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100.0%; Pred. No. 1.2e-42;
ative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (USSH ) US DEPT HEALTH & HUMAN SERVICES
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                                                                                                                                                     Claim 13; Page 49; 60pp; English.
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89US-00330446
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Best Local Similarity 100.
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       N-PSDB; AAQ85370
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30-MAR-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR73914 is the chemokine Human monocyte chemoattractant factor hMCP-1. It contains the meningitis related antigenic sequences (MRHAS) claimed in AAR73895 and AAR73807, which are recognised by a monoclonal antibody from the hybridoma Rubella virus (RV)-1. The claimed MRHAS peptides may be used in immunoassays to diagnose the presence of bacterial and/or viral meningitis agents in a sample, or in prophylactic and therapeutic meningitis Lreatments. The peptides may also be used as vaccines against (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 OPDAINAPVICCYNFINRKISVORLASYRRIISSKCPKEAVIFKTIVAKEICADPKOKWV 60
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                                                                                                                                                                                                                                                                  New peptide(s) and corresp. antibodies for the treatment of meningitis the peptide(s) corresp. to homologous antigenic sites on bacterial and viral agents and on chemokine(s), used for detecting and preventing meningitis.
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100.0%; Pred. No. 1.2e-42;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                           Claim 47; Fig 8/10; 98pp; English
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93US-00136117.
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(first entry)
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Best Local Similarity 100..
Then 76; Conservative
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                                                                                           (VALS/) VAN ALSTYNE
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                                                                                                                                                                  Van Alstyne D,
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28-SEP-1994;
                                               28-SEP-1993;
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29-AUG-1995
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human monocytes

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CC treatment of neoplasms and infections in humans. Short peptides derived from MCPs can be screened to identify those that can bind to the monocyte creeptor without stimulating a chemotactic response. These are copentially useful for treating inflammation associated with monocyte confiltration.

XX
SQ Sequence 99 AA;
Query Match
Best Local Similarity 100.0%; Score 405; DB 2; Length 99;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OPDAINAPUTCCYNFTNKKSVQRLASYRRITSSKCPKEAVIFKTIVAKEICADDFKQKWV 83

Db 24 QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADDFKQKWV 83
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61 ODSMDHLDKOTOTPKT 76

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Wed Sep

OM protein - protein search, using sw model

Run on:

August 30, 2004, 17:07:28 ; Search time 129 Seconds (without alignments) 185.353 Million cell updates/sec

07330446.PEP 405 1 gpdainapvtccynftnrki......gkwvgdsmdhldkgtgtpkt Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1297172 segs, 314612898 residues Searched: 1297172

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA:*

1: \cgn2_6/ptodata/1/pubpaa/USO'_PUBCOMB.pep:*
2: \cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*
4: \cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pep:*
4: \cgn2_6/ptodata/1/pubpaa/NSO6 NEW PUB.pep:*
5: \cgn2_6/ptodata/1/pubpaa/NSO7 NEW PUB.pep:*
6: \cgn2_6/ptodata/1/pubpaa/NSO7 NEW PUB.pep:*
7: \cgn2_6/ptodata/1/pubpaa/NSO7 NEW PUB.pep:*
7: \cgn2_6/ptodata/1/pubpaa/NSO7 NEW PUB.pep:*
8: \cgn2_6/ptodata/1/pubpaa/NSO7 PUBCOMB.pep:*
9: \cgn2_6/ptodata/1/pubpaa/NSO7 PUBCOMB.pep:*
11: \cgn2_6/ptodata/1/pubpaa/USO7 PUBCOMB.pep:*
12: \cgn2_6/ptodata/1/pubpaa/USO7 PUBCOMB.pep:*
13: \cgn2_6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*
14: \cgn2_6/ptodata/1/pubpaa/USO7 PUBCOMB.pep:*
15: \cgn2_6/ptodata/1/pubpaa/USO7 PUBCOMB.pep:*
16: \cgn2_6/ptodata/1/pubpaa/USO7 PUBCOMB.pep:*
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17: \cgn2_6/ptodata/1/pubpaa/USO7 PUBCOMB.pep:*
18: \cgn2_6/ptodata/1/pubpaa/USO7 PUBCOMB.pep:*
18: \cgn2_6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*
18: \cgn2_6/ptodata/1/pubpaa/USO7 NEW PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 5, Appli	Sequence 20, Appl	-	Sequence 1, Appli	Sequence 20, Appl	Sequence 5, Appli	Sequence 7, Appli	4	Sequence 14, Appl	Sequence 210, App	Sequence 16, Appl	Sequence 9, Appli	Sequence 5, Appli	Sequence 395, App	Sequence 9, Appli	
ΩI	US-09-195-457-5	US-09-792-793A-20	US-10-339-778-3	US-10-276-971-1	US-10-375-209A-20	US-10-332-038A-5	US-10-668-733-7	US-10-668-733-14	US-10-803-960-14	US-10-449-831A-210	US-08-927-939-16	US-09-920-137A-9	US-10-054-967-5	US-10-170-385-395	US-10-057-275-9	
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61 QDSMDHLDKQTQTPKT 76

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Sequence 4, Appli	'n	Sequence 9, Appli	equence 8,	е 6	equence 223	e 62,	equence 18,	2,	214	71,	e 71,	72,	e 72,	73,	e 73,	28,	e 28,	4,	() ()	263	equence 5,	e 5, Appl	e S	, Appl	e 19, App	equence 19, App	Sequence 19, Appl	equence 22, App	e 6,	
US-10-033-067-4	-141-965-	0-146-	S-10-293-705-	-10-137-65	-116-275-2	-10-440-464-	-10-764-649-1	9-778-	-10-449-	09-792-79	10-375-209A-	-792-793A-7	10-375-209A-	9-792-7	S-10-375-209A-	19-834-7	S-09-834-794A-	-10-339-	0-276-	-10-424-599-2	-09-920-	-10-057-	3-10-137-	9-792-793A-2	-10-646-770-1	-10-125-451-1	-263-1	-10-375-209A-	US-10-332-038A-6	
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16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

0; Gaps Query Match
100.0%; Score 405; DB 9; Length 76;
Best Local Similarity 100.0%; Pred. No. 4.6e-43;
Matches 76; Conservative 0; Mismatches 0; Indels US-US-195-497-5

Sequence 5, Application US/09195457

Patent No. US20020081623A1

GENERAL INFORMATION:

APPLICANT: JOSE, PETER J.

APPLICANT: GRIFFITES-JCHNSON, DAVID A.

APPLICANT: HGUAN, JOHN J.

TITLE OF INVENTION: CHEMOTACTIC CYTOKINE

FILE REFERENCE: 550-33

CURRENT APPLICATION NUMBER: US/09/195,457

CURRENT APPLICATION NUMBER: US/09/195,457

CURRENT APPLICATION NUMBER: 08/470,323

PRIOR APPLICATION NUMBER: PCT/GB94/02006

PRIOR FILING DATE: 1994-09-14

PRIOR FILING DATE: 1994-09-14

PRIOR APPLICATION NUMBER: GB 94086902.2

PRIOR APPLICATION NUMBER: GB 94086902.2

PRIOR FILING DATE: 1994-09-14

PRIOR APPLICATION NUMBER: GB 94086902.2

PRIOR APPLICATION NUMBER: GB 94086902.2

PRIOR APPLICATION NUMBER: GB 94086902.2

PRIOR SEQ ID NOS: 11

SEQ ID NO 5 ; TYPE: PRT ; ORGANISM: human US-09-195-457-5 JS-09-195-457-5

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RESULT 5
US-10-375-209A-20
Sequence 20, Application US/10375209A
Sequence 20, Application US/10375209A
Sequence 20, Application US/20030215421A1
Sequence 20, Application No. US20030215421A1
GENERAL INFORMATION:
APPLICANT: Cogglins, Philip
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS FOR TREATING SECONDARY TISSUE DAWAGE AND TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REPRESENCE: 25020-601E
CURRENT APPLICATION NUMBER: US/10/375,209A
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PATENTIN Ver. 2.0
SOFTWARE: PATENTIN Ver. 2.0
LENGTH: 76
LENGTH: 76
LENGTH: 76
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                                Sequence 1, Application US/10276971

Publication No. US20030162737A1

GENERAL INFORMATION:
APPLICANT: Egashira Kensuke
APPLICANT: Yashira Kensuke
APPLICANT: Yashiro Ikeda
APPLICANT: Yashiro Ikeda
TITLE OF INVENTION: Preventatives and Remedies for Pulmonary Hypertension
FILE REPERENCE: 2733 USOP
CURRENT APPLICATION NUMBER: US/10/276,971

CURRENT FILING DATE: 2002-11-20

NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV
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Best Local Similarity 100.0%; Pred. No. 4.6e-43;
Matches 76; Conservative 0; Mismatches 0; Indels
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, OTHER INFORMATION: Human Chemokine Polypeptide: MCP-1
US-10-375-209A-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Human
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US-10-332-038A-5
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                                                                                                            Sequence 20, Application US/09792793A

Patent No. US20020168370A1

AERIERAL INCRAMITION:
APPLICANT: McDonald, John R.
APPLICANT: Coggins, Philip
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601D
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601D
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601D
TITLE OF INVENTION: 0718RE 12011-02-22
NUMBER OF SEQ ID NOS: 93
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
LENGTH: 76
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APPLICANT: BOTRSEEIN, P.
APPLICANT: BYTISHIGES, T.
TITLE OF INVENTION: METHODS OF ENHANCING THE BIOCOMPATIBILITY OF AN IMPLANTABLE MEDIC
TITLE OF INVENTION: DEVICE
FILE REPREMENCY: UWOTL-1-20275
CURRENT APPLICATION NUMBER: US 60/347,560
PRIOR FILING DATE: 2002-01-10
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NOS: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 405; DB 9; Length 76; Best Local Similarity 100.0%; Pred. No. 4.6e-43; Matches 76; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: Human Chemokine Polypeptide: MCP-1 US-09-792-793A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/10339778 Publication No. US20030129214A1 GENERAL INFORMATION:
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61 QDSMDHLDKQTQTPKT
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Best Local Similarity 100.
Matches 76; Conservative
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US-10-339-778-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: homo sapien
                                                                         RESULT 2
US-09-792-793A-20
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; Publication No. US20040138422A1
; GENERAL INPORMATION:
; APPLICANT: Demotz et al.;
; TITLE OF INVENTION: SYNTHETIC CHEMOKINES LABELED AT SELECTED POSITIONS
; FILE REFERENCE: 29964/38772A
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 60/412,866
; RIOR FILING DATE: 2002-09-23
; PRIOR FILING DATE: 2002-09-23
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Offord, Robin
APPLICANT: Offord, Robin
APPLICANT: Offord, Robin
APPLICANT: Gerrerer, Hubert
APPLICANT: Gerrerer, Hubert
APPLICANT: Hartley, Oliver
ITILE OF INVENTION: Chemokine Receptor Modulators, Production and Use
FILE REPERENGE: 05504.271
CURRENT APPLICATION NUMBER: US/10/332,038A
CURRENT FILING DATE: 2003-05-06
FRICR FILING DATE: 2000-07-12
NUMBER OF SEQ ID NOS: 28
SEQ ID NOS: 28
SEQ ID NO 5
LENGTH: 76
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Best Local Similarity 100.0%; Pred. No. 4.6e-43;
Matches 76; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 405; DB 16; Length 76;
Best Local Similarity 100.0%; Pred. No. 4.6e-43;
Matches 76; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature; LOCATION: (75)...(75); LOCATION: (75)...(75); OTHER INFORMATION: The Lysine at position 75 is biotinylated US-10-668-733-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Synthetic peptide PEATURE:
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                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-332-038A-5
GENERAL INFORMATION:
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US-10-668-733-7
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RESULT 8 US-10-668-733-14

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Sequence 14, Application US/10668733

Publication No. US20040138422A1
GENERAL INFORMATION:
TITLE OF INVENTION: SYNTHETIC CHEMOKINES LABELED AT SELECTED POSITIONS
TITLE OF INVENTION: SYNTHETIC CHEMOKINES LABELED AT SELECTED POSITIONS
TITLE OF INVENTION: SYNTHETIC CHEMOKINES LABELED AT SELECTED POSITIONS
TITLE OF INVENTION: SYNTHETIC CHEMOKINES LABELED AT SELECTED POSITIONS
CURRENT APPLICATION NUMBER: US 60/412,866
PRIOR APPLICATION NUMBER: US 60/412,866
PRIOR FILING DATE: 2002-09-23
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PATENTIN VERSION 3.2
SSEQ ID NO 14
LENGTH: 76
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APPLICANT: White, John R.
APPLICANT: White, John R.
APPLICANT: Pells, Louis
APPLICANT: Li, Hacdong
APPLICANT: Li, Hacdong
APPLICANT: Li, Hacdong
APPLICANT: Li, Hacdong
APPLICANT: Stent L.
TILLE OF INVENTION: Novel Chemckine for Mobilizing Stem Cells
TILLE REPERENCE: PF497D2
CURRENT APPLICATION NUMBER: US/10/803,960
CURRENT FILING DATE: 2004-03-19
PRICR PILING DATE: 1999-01-06
PRICR APPLICATION NUMBER: US 60/006,051
PRICR PILING DATE: 1995-10-24
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 14
LENGTH: 78
LENGTH: 78
LENGTH: 78
LENGTH: 78
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100.0%; Score 405; DB 16;
Best Local Similarity 100.0%; Pred. No. 4.8e-43;
Matches 76; Conservative 0; Mismatches 0;
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100.0%; Score 405; DB 16;
Best Local Similarity 100.0%; Pred. No. 4.6e-43;
Matches 76; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , OTHER INFORMATION: Synthetic peptide US-10-668-733-14
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                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
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; ORGANISM: MCP-1
US-10-803-960-14
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US-10-803-960-14
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COMPUTER:
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                Sequence 210, Application US/10449831A
Publication No. US20040029179A1
GENERAL INFORMATION:
APPLICANT: Keentgen, Frank
TITLE OF INVENTION: Higher molecular weight entities and uses therefor
TITLE OF INVENTION: Higher molecular weight entities and uses therefor
CURRENT APPLICATION NUMBER: US/10/449,831A
CURRENT FILING DATE: 2003-05-30
PRIOR APPLICATION NUMBER: USSN 60/384878
PRIOR PILING DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 237
SOFTWARE: Patentin version 3.2
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APPLICANT: Grainger, David J.
APPLICANT: Grainger, David J.
APPLICANT: Tatalick, Lauen Marie
ITILE OF INVENTION: Compounds and methods to inhibit or
ITILE OF INVENTION: Compounds and methods to inhibit or
ITILE OF INVENTION: Compounds and methods to inhibit or
ITILE OF INVENTION: Compounds and methods to inhibit or
ITILE OF INVENTION: Compounds and methods to inhibit or
CURRENT APPLICATION NUMBER: 1897-09-11
NUMBER OF SEQ ID NOS: 83
SEQ ID NOS: 83
SEQ ID NO 16
LENGTH: 99
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US-08-927-939-16
Sequence 16, Application US/08927939
Publication No. US20010006640A1
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US-08-927-939-16
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Best Local Similarity
Matches 76; Conserve
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Human
JS-10-449-831A-210
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Sequence 9, Application US/09920137A Publication No. US20030049725A1 GENERAL INFORMATION:

US-09-920-137A-9

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1 QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV 60
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OLSEN, HENRIK S.
TITLE OF INVENTION: CHEMOKINE BETA-6 ANTAGONISTS
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 99;
APPLICANT: Coleman, Roger
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Milde, Craig G
TITLE OF INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 405; DB 10; Best Local Similarity 100.0%; Pred. No. 6.3e-43; Matches 76; Conservative 0; Mismatches 0;
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ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FESCESQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/920,137A
FILING DATE: US/08/920,137A
ATTORNEY/AGENT INFORMATION:
NAME: LUCHER, BATBATA J.
REGISTRATION NUMBER: 33,954
REFERENCE/DOKET UNMBER: PF-0027 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
US-10-054-967-5
; Sequence 5, Application US/10054967
; bublication No. US20030059874A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: KREIDER, BRENT L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
TENGTH: 99 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 ODSMDHLDKQTQTPKT 76
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                                                                                                                                                                                                                                                                                                                               E: Diskette
IBM Compatible
                                                                                                                                                                                                                                                                      ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: MCP-1
                                                                                                                                                                                                     Palo Alto
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24 QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCFKBAVIFKTIVAKEICADPKQKWV 83
                                                                  24 QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKBAVIFKTIVAKBICADPRQKWV 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 OPDAINAPVICCYNFINRKISVORLASYRRITSSKCPKEAVIFKTIVAKEICADPKOKWV
                       1 OPDAINAPVICCYNFINRKISVORLASYRRIISSKCPKBAVIFKTIVAKEICADPKOKWV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/057,275
FILING DATE: 25-dan-2002
PRIOR APPLICATION NUMBER: US/08/390,740A
PLICATION DATA:
APPLICATION NUMBER: US/08/390,740A
PLICATION NUMBER: US/08/390,740A
PLICATION NUMBER: US/08/390,740A
REGISTRATION NUMBER: 33,954
REGISTRATION NUMBER: 33,954
REGISTRATION NUMBER: PF-0027 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-65-055
TELEPHONE: 415-65-055
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
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                                                                                                                                                 61 Орѕмрнгркототркт
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US-10-057-275-9
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100.0%; Score 405; DB 12; Length 99;
Best Local Similarity 100.0%; Pred. No. 6.3e-43;
Matches 76; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 99;
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 405; DB 12; Best Local Similarity 100.0%; Pred. No. 6.3e-43; Matches 76; Conservative 0; Mismatches 0;
                                                                                         FILING DATE: 25-Jan-2002

FLIASSIFICATION CADACOMD

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/995,156

FILING DATE: 19-DEC-1997

ATTORES/AGENT INPORMATION:

NAME: STEFFE, ERIC K

REGISTRATION NUMBER: 36,688

REGISTRATION NUMBER: 36,688

REGISTRATION INPORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFOGRATION:
GENERAL INFOGRATION:
APPLICANT: Ward, Neil Raymond
APPLICANT: Man, On
APPLICANT: Harris, Robert Alan
APPLICANT: Harris, Robert Alan
APPLICANT: Binley, Katie Mary
APPLICANT: Binley, Katie Mary
APPLICANT: RAYDER, William Nigel
APPLICANT: RAYDER, William Nigel
APPLICANT: Kingsman, Susan Mary
APPLICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DENGTH: 99 amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-054-967-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 395, Application US/10170385 Publication No. US20030203372A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 Орѕмрнгркототркт 76
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CORGANISM: Homo Sapiens
US-10-170-385-395
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GenCore version 5.1.6

Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 30, 2004, 16:52:21 ; Search time 24 Seconds

(without alignments)

164.889 Million cell updates/sec
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Title: 07330446.PEP Perfect score: 405 Sequence: 1 qpdainapvtccynftnrki......qkwvqdsmdhldkqtqtpkt 76

Scoring table: BLOSUM62 Gapext 0.5

Searched: 141681 segs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	homo s	Q9myn4 macaca fasc	P42831 sus scrofa			oryc		homo	ม STW	homo	homo	s sns	Q99616 homo sapien	_	Q09141 bos taurus		-			cav		ratt	Q9z121 mus musculu	ยาแ	pos t	homo	P10147 homo sapien	homo	gallu	13236 h smal	P46632 oryctolagus	50230 rattue	14	
SUMMARIES	ID	SY02 HUMAN	SY02 MACFA	SY02 PIG	SY02 CANFA	MCPA_BOVIN	SY02_RABIT	MCPB_BOVIN	SY07_HUMAN	SY12_MOUSE	EOTA_HUMAN	SY08 HUMAN	SY08_PIG	SY13 HUMAN	SY02_MOUSE	SY08_BOVIN	SY02_RAT	SY02_CAVPO	EOTA_RAT	EOTA_MOUSE	EOTA_CAVPO	SY07_MOUSE	SY07_RAT	SY08_MOUSE	SY24 MOUSE	REG1_BOVIN		<u>ا</u> ا		SY04_CHICK		SY04 RABIT	SY04 RAT	SYD1_RAT	-
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	Score		394	337	331	315	314	308	287	284	273	268	261	253.5	252	247	241	236	221	218	214	202	202	177		148.5	4	4,	137	m	135.5	ന	m	131	
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SYD1_MOUSE SY04_MOUSE	SY21_HUMAN SY03_RAT	SY14_HUMAN SYD1_HUMAN	SY03 MOUSE	SY05_SIGHI	SY18_HUMAN	SY05_CAVPO	SY05_BOVIN
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ALIGNMENTS

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MUTAGENESIS
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    RY MEDLINE=22388257; PubMed=12477932;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Collings I.S., Grouse L.H., Derge J.G.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
BA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
BA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gabuarathe P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gabuarathe P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gabus R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
R Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
R Generation and initial analysis of more than 15,000 full-length
R Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-91301709; PubMed-2071154;
Rollins B.J., Morton C.C., Ledbetter D.H., Eddy R.L. Jr., Shows T.B.;
"Assignment of the human small inducible cytokine A2 gene, SCYA2
(encoding JE or MCP-1), to 17q11,2-12: evolutionary relatedness of cytokines clustered at the same locus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Robinson E.A., Yoshimura T., Leonard B.J., Tanaka S., Griffin P.R., Shabanowitz J., Hunt D.F., Appella E., "Complete amino acid sequence of a human monocyte chemoattractant, a putative mediator of cellular immune reactions.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 29-53 AND 82-92.

MEDLINE-90211336; PubMed=232286;.

MEDLINE-90211336; PubMed=232286;.

MEDLINE-90211336; PubMed=232286;.

MIGHATIFICATION OF The monocyte chemotractic protein from human osteosarcoma cells and monocytes: detection of a novel N-terminally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

PEDLINE-20744005; PubMed=10918580;
Finzer P., Soto U., Delius H., Patzelt A., Poustka A., Coy J.F.,
zur Hausen H., Roesl F.;
zur Hausen H., Rossl F.;
Charactriptional regulation of the
monocyte-chemoattractant protein-1 (MCP-1) gene in tumorigenic and
non-tumorigenic HPV 18 positive cells: The role of the chromatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A., Rajkumar N., Toth B.J., Yi Q., Nickerson D.A.; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
                                                            "The expression of monocyte chemotactic protein (MCP-1) in human vascular endothelium in vitro and in vivo."; Wol. Cell. Biochem. 126:61-68(1993).
MEDLINE=94150478; PubMed=8107690;
Li Y.S., Shyy Y.J., Wright J.G., Valente A.J., Cornhill J.F.,
Kolattukudy P.E.;
                                                                                                                                                                                                               in monocyte chemoattractant protein-1 (MCP-1).";
Exp. Med. Biol. 305:47-56(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            putative mediator of cellular immune reactions.";
Proc. Natl. Acad. Sci. U.S.A. 86:1850-1854(1989).
                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=92095166; PubMed=1661560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      structure and AP-1 composition.";
Oncogene 19:3235-3244(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 24-99.
MEDLINE=89184525; PubMed=2648385;
                                                                                                                                                                                                      Yoshimura T., Leonard E.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                       Genomics 10:489-492(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                        "Human monocyte
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Weber M., Uguccioni M., Baggiolini M., Clark-Lewis I., Dahinden C.A.; "Deletion of the NA2-terminal residue converts monocyte chemotactic protein 1 from an activator of basophil mediator release to an eosinophil chemoattractant.";
                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).
MEDLINE=97143315; PubMed=8989326;
Lubkowski J., Bujacz G., Domaille P.J., Handel T.M., Wlodawer A.;
"The structure of MCP-1 in two crystal forms provides a rare example of variable quaternary interactions.";
Nat. Struct. Biol. 4:64-69(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRUCTURE BY NMR.
MEDLINE=96234959; PubMed=8639605;
Handel T.M., Domaille P.J.;
"Heteronuclear (1H, 13C, 15N) NMR assignments and solution structure of the monocyte chemoattractant protein-1 (MCP-1) dimer.";
Blochemistry 35:6569-6584(1996).
                                                                                                                              MEDINE-91312872; Pubmed-1857712; Gronenborn A.M., Clore G.M.; Modeling the three-dimensional structure of the monocyte chemo-modeling the three-dimensional structure of the monocyte chemo-actuate and activating protein MCAF/MCP-1 on the basis of the solution structure of interleukin-8.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kim K.-S., Rajarathnam K., Clark-Lewis I., Sykes B.D.; "Structural characterization of a monomeric chemokine: monocyte
processed form.";
Biochem. Biophys. Res. Commun. 167:904-909(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EFFECT OF DELETION OF N-TERMINAL RESIDUES.
MEDLINE=96195223; PubMed=8627182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97053697; PubMed=8898111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, M31626; AAA36330.1; --
EMBL, M30816; AAA36330.1; JOINED.
EMBL, M31625; AAA36330.1; JOINED.
EMBL, M24545; AAA18164.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Exp. Med. 183:681-685(1996).,
                                                                                                                                                                                                                                                                                                                Protein Eng. 4:263-269(1991).
                                                                                                       3D-STRUCTURE MODELING
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Protein: United R. P. Studer C., Utfer R.,

RT "Cloning and expression of rhesus monkey monocyte chemoattractant

RT "Cloning and expression of rhesus monkey monocyte chemoattractant

RT Studer C., Utfer R.,

RT "Cloning and expression of rhesus monkey monocytes and basophils

Submitted (ARR-2000) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: Chemotactic factor that attracts monocytes and basophils

similarity)

-!- SUBCRILULAR LOCATION: Secreted.

-!- SUBCRILULAR LOCATION: Secreted.

-!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.

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The European Bioinformatics Institute. There are no restrictions on its

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modified and this statement is not removed. Usage by and for commercial

cut send an email to license@isb-sib.ch).
                                                                                              1 OPDAINAPVICCYNFINRKISVORLASYRRIISSKCPKEAVIFKTIVAKEICADPKOKWV 60
                                                                                                                        24 QPDAINAPVICCYNFINRKISVQRLASYRRIITSSKCPKEAVIFKTIVAKEICADPKQKWV 83
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
protein 1) (MCP-1) (Monocyte chemoattractant protein-1).
CCL2 OR SCYA2 OR MCP1.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and Macaca mulatta (Rhesus macaque).
Bukaryota, Metazca; Chordata; Craniata; Vertebrata; Euteleostomi; Carnopithecinae; Macaca.
Cercopithecinae; Primates; Catarrhini; Cercopithecidae;
                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SPECIES=M.fascicularis,
Studer C., Urfer R.;
"Cloning and expression of cynomolgus monkey chemoattractant
                      Length 99;
                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein-1.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF276081; AAF81899.1; --
EMBL; AF25343; AAF67756.1; --
EMSP; P13500; 1DOK.
InterPro; IPR000827; CC chemkine sml.
InterPro; IPR00081; Chemokine II.
InterPro; IPR008097; Fractalkine.
Pfam; PF00748; ILB; 1.
PRINTS; PR01721; FRACTALKINE.
SWART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL CYTOKINES CC; 1.
PROSITE; PS0472; SMALL CYTOKINES CC; 1.
CYTOKINE; CHEMOTAXIS; SIGNAL; BY SIMILARITY.
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
SMALL INDUCIBLE CYTOKINE
                  100.0%; Score 405; DB 1; 100.0%; Pred. No. 1.5e-40; iive 0; Mismatches 0;
                                                                                                                                                                    Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES=M.mulatta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                        MACFA
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                                                                                                                                                                                                            83
                                                                                                                                                                          1 OPDAINAPVICCYNFINRKISVORLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV
                                                                                                                                                                                               24 QPDAINAPVTCCYNFINRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPRQKWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neutrophils.
--- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
--- SUBCELLULAR LOCATION: Secreted.
--- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=94183284; PubMed=7510962;
Hosang K., Knoke I., Klaudiny J., Wempe F., Wuttke W., Scheit K.H.;
"Porcine luteal cells express monocyte chemoattractant protein-1
(MCP-1): analysis by polymerase chain reaction and cDNA cloning.";
Biochem. Biophys. Res. Commun. 199:962-968(1994).
                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Small inducible cytokine A2 precursor (CCL2) (Monocyte chemotactic protein 1) (MCP-1) (Monocyte chemoattractant protein-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Brain,
Zach O.R.F.;
Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Chemotactic factor that attracts monocytes, but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa (Pig).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                              BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCMC. . .) (POTENTIAL)

433CB88C64EE7A4F CRC64;
                                                                                                                                              .,
PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).
                                                                                                                                            1; Indels
                                                                                                               1; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z48479; CAA88370.1; -.

EMBL; X79416; CAA55945.1; -.

FIR; UCC136; UCC136.

HSSP; P13500; 1D0M.

InterPro; IFR0018011; Chēmokine_ILē.

Ffan; PF00046; Li8; I.Chēmokine_ILē.

Ffan; PF00046; Li8; I.CYTOKINES_CC; I.

PROSITIS; PS00472; SMALL, CYTOKINES_CC; I.

CYCOKINE; Chemotaxis; Sīgnal; Inflammatory response; Pyrrolidone carboxylic acid.

SIGNAL

CHAIN

24 SPMALL; INDUCIBLE CYTOKINE ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
SMALL INDUCIBLE CYTOKINE
                                                                                                              Score 394; DB 1;
Pred. No. 3e-39;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                       99 AA
                                59
75
37
11007 MW;
                                                                                                              97.3%;
ilarity 98.7%;
Conservative
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                                                                                                                                                                                                                                                                      84 ODSMDHLDKOIOTPK 98
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                                                                                                                             Local Similarity
les 74; Conserv
                              34
35
37
99 AA;
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                                                                                                                                                                                                                                                                                               RESULT 3
SY02 PIG
TD SY02 PIG
P42831;
                                DISULFID
DISULFID
CARBOHYD
SEQUENCE
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   MOD_RES
   STILL
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PYRROLIDONE CARBOXYLIC ACID (BY

MOD_RES

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QPDAINAPVICCYNFINRKISVQRLASYRRIISSKCPKEAVIFKIIVAKEICADPKQKWV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 QPDAIISPVTCCYTLINKKISIQRLASYKRVTSSKCPKEAVIFKTVLNKEICADPKQKWV 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
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MEDLINE-92181448; PubMed-1543494;
Nempe F., Einspanier R., Scheit K.H.;
"Characterization by cDNA cloning of the mRNA of a new growth factor farm bovine seminal plasma: acidic seminal fluid protein.";
Biochem. Biophys. Res. Commun. 183:232-237(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUB-Seminal plasma; Manabal 1721821; Manabal 1721821; Manabal 1721821; Member 17. PubMed=1721821; Member 17. PubMed=1721821; Member 17. Memb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94338337; PubMed=8060303; Wempe F., Kuhlmann J.K., Scheit K.H.; "Characterization of the bovine monocyte chemoattractant protein-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-1992 (Rel. 24, Last sequence update)
10-0cT-2003 (Rel. 42, Last annotation update)
Monocyte chemotactic protein 1A precursor (MCP-1A) (MCP-1) (Acidic
seminal fluid protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine)...

Bukaryota, Medazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butharia, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 202:1272-1279(1994).
-!- FUNCTION: Chemotactic factor that attracts monocytes, but not neutrophils.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
                                                                                                                                      (BY
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 331; DB 1; Length 101;
                                                                                        SMALL INDUCIBLE CYTOKINE A2. PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Indels
                                                                                                                                                                                                                                                                                                                                            CDD7E2B1901A7267 CRC64;
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                                                                                                                                                                                                                                    BY SIMILARITY.
BY SIMILARITY.
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                                                   BY SIMILARITY
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01-DEC-1992 (Rel. 24, Last seqn
10-OCT-2003 (Rel. 42, Last anno
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                                                                                                                                                                                                                                                                                                                                            101 AA; 11121 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                         81.7%;
80.5%;
acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62; Conservative
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     carboxylic
     Pyrrolidone
                                              SIGNAL
          STTTTTT
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SO THE STANK SERVICE OF THE SERVICE 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
R EMBL; M84602; AAAL.

JR PIR; A39296; A39296.

BR HSSP; P13500; 1DDM.

DR InterPro; IPR010817; CC chemkine sml.

DR InterPro; IPR010811; Chēmokine_IIB.

DR SMART; SM00199; SCY; 1.

DR SMART; SM00199; SCY; 1.

DR Cytokine; Chemciaxis; Signal; Pyrrolidone carboxylic acid.

FT CAIM 24 99 MONOCYTE CHEMOTACTIC PROTEIN IA.

FT CAIM 24 99 MONOCYTE CHEMOTACTIC PROTEIN IA.

FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).

THEND 34 59 BY SIMILARITY.

THEND 34 59 BY SIMILARITY.

THEND 35 59 BY SIMILARITY.

THEND 36 59;

THEND 37 51 ILENGTH 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
10-DCT-2003 (Rel. 42, Last annotation update)
Small inducible cytokine A2 precursor (CCL2) (Monocyte chemotactic protein 1) (MCP-1) (Monocyte chemoattractant protein-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=New Zealand white; TISSUE=Spleen;
MEDLINE=91225489; PubMed=2026877;
Yoshimura T., Yuhki N.;
"Neutrophil attractant/activation protein-1 and monocyte chemoattractant protein-1 in rabbit. cDNA cloning and their chemoattractant protein-1 in rabbit. cDNA cloning and their cypression in spleen cells.";
J. Immunol. 146.3483-348 [1991)
-!- FUNCTION: Chemotactic factor that attracts monocytes, but not neutrophils.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
77.8%; Score 315; DB 1; Length 99;
Best Local Similarity 73.3%; Pred. No. 5.1e-30;
Matches 55; Conservative 13; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 AA
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InterPro; IPR001811; Chemokine_ILB.
Pfam; PF00048; ILB; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 QDSMDHLDKQTQTPK 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||:::|:|
QDSINYLNKKNQTPK 98
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SY02 RABIT
ID SY02 RABIT
AC P28292;
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WEDLINE=95034774; PubMed=7947749;

WEDLINE=95034774; PubMed=7947749;

Prooft P. Wuyte A., Lenaerts J.-P., van Damme J.;

Prooft P., Wuyte A., Lenaerts J.-P., van Damme J.;

Prooft P., Wuyte A., Lenaerts J.-P., van Damme J.;

Purification, sequence analysis, and biological characterization of a second bovine monocyte chemotactic protein-1 (Bo MCP-1B).";

La second bovine monocyte chemotactic factor that attracts monocytes, but not neutrophils. Augments monocyte anti-tumor activity. Also induces the release of geladinase B. This protein can bind heparin.

C.-I. PTM: The N-terminus is blocked.

C.-I. SIMILARITY: Belongs to the intercrine beta (chemokine CC) family. RSP: PISSO0; 118; 11.

RINESP: ILB: 11.

RESP: PRO0481; LB: 11.

RESP: PRO0481; LB: 11.

RESP: PRO0481; LB: 11.

RESP: PRO0481; LB: 11.

RESP: PRO0481; CC, Chemkine Sml.

RESP: RESP: PRO0482; CC, Chemkine Sml.

RESP: PRO0481; CC, Chemkine Sml.

RESP: RESP: PRO0482; CC, Chemkine Sml.

RESP: PRO0482; CC, Chemkine Sml.

RESP: PRO0482; CC, Chemkine Sml.

RESP: PRO0482; CC, Chemkine Sml.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 QPDAVNSPVTCCYTFTNKTISVKRLMSYRRINSTKCPKBAVIFMTKLAKGICADPKQKMV 83
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SWART; SM00199; SCY; 1.

PROSITE; PS00472; SMALL CYTOKINES CC; 1.

Cytokine; Chemotaxis; Signal; Inflammatory response; Glycoprotein;

Pyrrolidone carboxylic acid.

SIGNAL BY SIMILARITY.

CHAIN 24 125 SWALL INDUCIBLE CYTOKINE A2.

MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.1-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Monocyte ofhemicatic 'protein IB (MCP-1B) (Fragment).
Elso taurus (Bovine).
Elso taurus (Bovine).
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
                                                                                                                                     BY SIMILARITY.
SMALL INDUCIBLE CYTCKINE A2.
PYRROLIDONE CARBOXYLIC ACID (BY
SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
M. 24C3A542CB6A47EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 77.5%; Score 314; DB 1; Length 125; Best Local Similarity 75.0%; Pred. No. 8.6e-30; Matches 57; Conservative 10; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tch 76.0%; Score 308; DB 1; Length 74; al Similarity 75.3%; Pred. No. 2.5e-29; 55; Conservative 8; Mismatches 10; Indels
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FAAF72B970EB16E3 CRC64;
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35 75 BY
40 40 N-1
55 58 N-1
112 112 N-1
125 AA; 13776 MW;
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10 50
74 AA; 8360 MW;
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ID MCPB BOVIN
AC P80343;
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Best Local S
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[8] STRUCTURE BY NMR. 54; MOD_RES DISULFID DISULFID CARBOHYD HELIX SEQUENCE CONFLICT Query Match STRAND SIGNAL STRAND STRAND Matches TURN 셤 ठ g ò MEDLINE=9230885; PubMed=1613466; van Damme J., Prossiber G.; van Damme J., Prossi P., Lenaerts J.-P., Opdenakker G.; structural and functional identification of two human, tumor-derived monocyte chemotactic proteins (MCP-2 and MCP-3) belonging to the SEQUENCE FROM N.A.
MEDLINE=93305913; PubMed=8318676;
Minry A., Chalon P., Guillemot J.C., Kaghad M., Liauzun P.,
Magazin M., Miloux B., Minty C., Ramond P., Vita N., Lupker J.,
Shire D., Ferrara P., Caput D.;
"Molecular cloning of the MCP-3 chemokine gene and regulation of its MEDIINE=97263733; PubMed=9109648; Meunier S., Bernara P., Darbon H.; Meunier S., Bernassau J.-M., Guillemot J.-C., Ferrara P., Darbon H.; "Determination of the three-dimensional structure of CC chemokine monocyte chemoattractant protein 3 by 1H two-dimensional NMR SEQUENCE FROM N.A. MEDLINE=94375065; PubMed=7916328; Opdenakker G., Fiten P., Nys G., Froyen G., van Roy N., Speleman F., σĘ 01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Small inducible cytokine A7 precursor (CCL7) (Monocyte chemotactic
protein 3) (MCP-3) (Monocyte chemoattractant protein 3) (NC28).
CCL7 OR SCYA7 OR MCP3.
Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606; SEQUENCE FROM N.A., AND SEQUENCE OF 31-67 AND 71-99.
MEDLINE-93213290; PubMed-8461011;
Opdenakker G., Froyen G., Fiten P., Proost P., van Damme J.;
Human moncyte chemotactic protein-3 (MCP-3): molecular cloning
the cDNA and comparison with other chemokines.";
Biochem. Biophys. Res. Commun. 191:535-542(1993). Kim K.-S., Rajarathnam K., Clark-Lewis I., Sykes B.D.;
"Structural characterization of a monomeric chemokine: monocyte
chemoattractant protein-3.";
FEBS Lett. 395:277-282(1996). Laureys G., van Damme J.; cloning, sequence analysis, and assignment to the C-C chemokine gene cluster on chromosome Jang J.S., Kim B.E.; Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases. 99 A.A. Eur. Cytokine Netw. 4:99-110(1993) STRUCTURE BY NMR, AND SUBUNIT. MEDLINE=97053697; PubMed=8898111; spectroscopy."; Biochemistry 36:4412-4422(1997) 01-DEC-1992 (Rel. 24, Created) chemokine family."; J. Exp. Med. 176:59-65(1992) SEQUENCE OF 24-99 FROM N.A. 17q11.2-q12."; Genomics 21:403-408(1994) 63 SMDHLDKQTQTPK 75 SISHLDKKNQXPK 73 STANDARD; TISSUE=Osteosarcoma; SECUENCE OF 30-99. STRUCTURE BY NMR. SY07_HUMAN P80098; expression.

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                                                                                                                                                                                             -!- SUBUNIT: Monomer.
-!- SUBCELLUAR LOGATION: Secreted.
-!- PTM: O-glycosylated.
-!- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
Kwon D., Lee D., Sykes B.D., Kim K.-S.;
Submitted (AUG-1998) to the PDB data bank.
-!- FUNCTION: Chemotactic factor that attracts monocytes and
eosinophils, but not neutrophils. Augments monocyte anti-tumor activity, Also induces the release of gelatinase B. This protein can bind heparin. Binds to CCR1, CCR2 and CCR3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00048; IL8; 1.
SMART: SW00199; SCY; 1.
PROSITE; PS00472; SMALL CYTOKINES CC; 1.
Cytokine; Chemotaxis; Heparin-binding; Glycoprotein; Signal; Inflammatory response; 3D-structure; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC. . .) (POTENTIAL).
T -> K (IN REF. 5).
MISSING (IN REF. 5).
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Pred. No. 9.6e-27;
4; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMALL INDUCIBLE CYTOKINE A7. PYRROLIDONE CARBOXYLIC ACID.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X72308; CAA51055.1; ALT INIT. EMBL; X72309; .; NOT ANNOTATED CDS. EMBL; X1087; CAA50406.1; ALT INIT. EMBL; X71087; CAA50406.1; ALT INIT. EMBL; X1087; CAA50405.1; ALT INIT. EMBL; AF043338; AAC03538.1; -. PDB; 1NCV; 15-OCT-99. PDB; 1BO0; 10-OCT-99. Genew; HGNC: 10634; CCL7.
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99 AA;
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response; Polymorphism

EMBL, AP065930,
1 HSSP, P13500, 1DDL.
R MSD; MGT:108224; CC112.
R MSD; MGT:108224; CC112.
DR InterPro; IPR001811; Cfemokine_IE8.
DR Pfam; PF00048; IL8; 1.
DR PROSITE; PS00472; SMALL CYTOKINES CC; 1.
DR PROSITE; PS00472; SMALL CYTOKINES CC; 1.
CYTOKine; Chemotaxis; Signal; Inflammatory response; Polymorph.
SMALL INDUCIBLE CYTOKINE A12.
SMALL INDUCIBLE CYTOKINE A12.
CATMILARITY.
CATMILARITY.
CATMILARITY.
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DR X A DR

AF065936; AAF15386.1; -. AF065937; AAF15387.1; -. AF065938; AAF15388.1; -.

EMBL; EMBL; EMBL;

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SB102284FF4CC3DBF CRC64;

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EXECUTION E. FRUM N.A.

THE SEQUENCE FRUM N.B.

RA THE STAIN—S10.8/J, BAIBAC = 10438970,

THE STAIN—S1370037; PubMed=10438970,

THE STAIN—S1370037; PubMed=10438970,

THE STAIN—S1370037; PubMed=10438970,

RA Blankenhorn B.P.; MR R.Z., Zachary J.F., Doerge R.W.;

RA Blankenhorn B.P.; MR R.Z., Zachary J.F., Doerge R.W.;

RA Candidates for eae7, a locus controlling susceptibility to monophasic and dates for eae7, a locus controlling susceptibility to monophasic remitting/nonrelapsing experimental allergic encephalomyelitis.";

J. Immunol. 163:2562-2266(1999).

C. Immunol. 163:262-2266(1999).

C. Immunol. 163:262-2266(1
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It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
SY12_MOUSE STANDARD; PRT; 104 AA.
062401; 090YD6;
01-NOV-1997 (Rel. 35, Created)
15-MAR-2004 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Small inducible cytokine Al2 precursor (CCL12) (Monocyte chemotactic proterin S) (MCP-S) (M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jia G.-Q., Gonzalo J.A., Lloyd C., Kremer L., Lu L., Martinez A.C., Wershil B.K., Gutierrez-Ramos J.C.;
Distinct expression and function of the novel mouse chemokine monocyte chemotactic proctein-5 in lung allergic inflammation.";
J. Exp. Med. 184:1939-1951(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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MEDLINE=97079149; Pubmed=8920881;
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MEDLINE-S6181789; PubMed-8597956;
Garcia-Zepeda E.A., Rothenberg M.E., Ownbey T.R., Leder P.,
Luster A.D.;
"Human ecravin is a specific chemoattractant for eosinophil cells and
provides a new mechanism to explain tissue eosinophilia.";
Nat. Med. 2:449-456(1996).
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                                                                          2 PDAINAPVICCYNFINRKISVQRLASYRRITSSKCPKEAVIFKTIVAKBICADPKOKWVQ
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                                                                                                                                                                                                                                                                                EGTA HUMAN STANDARD; PRT; 97 AA.
PSIG11, FGSR7; Q92491;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
115-MAR-2004 (Rel. 43, Last annotation update)
Ectaxin precursor (Small inducible cytokine All) (CCL11) (Eosinophil CCL11 OR SCYA11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mackay C.R.;
"Cloning of the human eosinophil chemoattractant, eotaxin. Expressic receptor binding, and functional properties suggest a mechanism for the selective recruitment of eosinophils.";
J. Clin. Invest. 97:604-612(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Small intestine;
MEDLINE-96205964; PubMed-8631813;
Kitaura M., Nakajima T., Imai T., Harada S., Combadiere C.,
Tiffany H.L., Murpima P.M., Yoshie O.;
"Molecular cloning of human eotaxin, an eosinophil-selective CC chemokine, and identification of a specific eosinophil eotaxin receptor, CC chemokine receptor 3.";
J. Biol. Chem. 271:7725-7730(1996).
                                     ;
Length 104;
                                     8; Indels
70.1%; Score 284; DB 1;
68.1%; Pred. No. 2.3e-26;
iive 15; Mismatches 8
                 Local Similarity 68.1
les 49; Conservative
                                                                                                                                                 73
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84 NSINHLDKTSQT 95
                                                                                                                                                   62 DSMDHLDKOTQT
                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
   Query Match
                                                                                                                                                                                                                                              RESULT 10
EOTA HUMAN
                         Best Loca
Matches
                                                                                                                                                                                                                                                                                      8
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EMBL, U50712; AAB50053.1; -.
EMBL, U66670; AAB49424.1; -.
EMBL, AP065934; AAF15384.1; -.
EMBL, AF065935; AAF15385.1; -.

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0; Gaps

67.4%; Score 273; DB 1; Length 97; ilarity 68.6%; Pred. No. 4.1e-25; Conservative 12; Mismatches 10; Indels

Local Similarity es 48; Conser Query Match Best Loca Matches Altschul S.P., Telungold E.A., Grouse L.H., Derge J.G.,
Rausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Rlausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buercow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Carninci P., Hulyk S.W.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gabb S.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Human and mouse CDNA sequences "J. Norsk Chart N.A.) "Genomic organization, complete sequence, and chromosomal location of the gene for human ectaxin (SCYAll), an ecsinophil-specific CC STRUCTURE BY NMR.
MEDILINE=98380465; PubMed=9712872;
MEDILINE=98380465; PubMed=9712872;
Crump M.P., Rajarathnam K., Kim K.S., Clark-Lewis I., Sykes B.D.;
"Solution structure of eotaxin, a chemokine that selectively recruits
eosinophils in allergic inflammation.";
J. Biol. Chem. 273:2247-22479(1998).
-!- FUNCTION: In response to the presence of allergens, this protein
directly promotes the accumulation of eosinophils, a prominent
feature of allergic inflammatory reactions. Binds to CCR3.
-!- SUBCELLULAR LOCATION: Secreted. TISSUB-Lung,
MEDLINE=97445071; PubMed=9299399;
Mein H., Schlueter C., Kulke R., Christophers E., Schroeder J.-M., "Genomic organization, sequence, and transcriptional regulation of "Delayed production of biologically active O-glycosylated forms of human ectaxin by tumor-necrosis-factor-alpha-stimulated dermal Garcia-Zepeda B.A., Rothenberg M.B., Weremowicz S., Sarafi M.N., Morton C.C., Luster A.D.; MEDLINE-98237580; PubMed-9578468; Noso N., Bartels J., Mallet A.I., Mochizuki M., Christophers E., [4] SEQUENCE FROM N.A., SEQUENCE OF 60-65 AND 75-88, AND VARIANTS. MEDLINE=96374440; PubMed=8780731;
Bartels J., Schlueter C., Richter E., Noso N., Kulke R.,
Christophers E., Schroeder J. M.;
"Human dermal fibroblasts express ectaxin: molecular cloning,
expression, and identification of ectaxin sequence variants."
Biochem. Biophys. Res. Commun. 225:1045-1051(1996). numan and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). the human ectaxin gene."; Biochem. Biophys. Res. Commun. 237:537-542(1997). TISSUE=Lung; MEDLINE=22388257; PubMed=12477932; Eur. J. Biochem. 253:114-122(1998) TISSUE=Placenta; MEDLINE=97312708; PubMed=9169149; Genomics 41:471-476(1997). CARBOHYDRATE-LINKAGE SITE. SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. Schroeder J.-M.; TISSUE-Foreskin; rissum=Blood; Fibroblasts. chemokine."

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INDUCTION: By TNF-alpha, interleukin-1 alpha and interferon gamma. PTM: O-LINKED GIYCAN CONSIGNS OF A GAL-GALINK DISACCHARIDE WHICH IS MOPIFIED WITH UP TO 2 SIALIC ACID RESIDUES.
SIMILARITY: Belongs to the intercrine beta (chemokine CC) family. DATABASE: NAME=R&D Systems' Cytokine source book: SCYA11; WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=196".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A GO; GO: 000609; F: chemokine activity; TAS.

A GO; GO: 0006099; F: chemokine activity; TAS.

A GO; GO: 0006099; F: chemotaxis; TAS.

B GO; GO: 0006395; P: chemotaxis; TAS.

C GO; GO: 0006995; P: chemotaxis; TAS.

C GO; GO: 00069914; P: response to radiation; TAS.

C GO; GO: 0009615; P: response to radiation; TAS.

C GO; GO: 0009615; P: response to viruses; TAS.

C GO; GO: 0009615; P: response to viruses; TAS.

C GO; GO: 0009615; P: response to viruses; TAS.

C GO; GO: 0009615; P: signal transduction; TAS.

C GO; GO: 000165; P: signal transduction; TAS.

C DEPPRO; PRR000191; C-chemkine_sml.

C SMART; SMO0199; SCY; L.

C SME PROSITE; PSO0472; SMALL CYTOKINES CC; L.

C SMART; PSO0472; SMALL CYTOKINES CC; L.

C SMART; CASPONSE; POlymorphism; 3D-structure.
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FTIG=VAR 001634.

A -> T (IN CLONE 53).

FTIG=VAR 001635.

R -> S (IN CLONE 34).

FTIG=VAR 001636.

K -> R (IN CLONE 53).

FTIG=VAR 001637.
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L -> P (IN CLONE 34).
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EMBL, U44780; AAC50369.1; --
EMBL, D49372; BAA08370.1; --
EMBL, Z69291; CAA99258.1; --
EMBL, Z75668; CAA99997.1; --
EMBL, Z75669; CAA99998.1; --
EMBL, Z92709; CAB07027.1; --
EMBL, BCO17850; AAH17850.1; --
EMBL, JC4912, JC4912.
PDB; LECT, 13.4M-99.
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MIM; 60
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                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00048; ILB; 1.
SMART; SMO199; SCY; 1.
PROSTIE; PS00472; SCALL CYTOKINES CC; 1.
Cytokine; Chemotaxis; Signal; Heparin-binding; Inflammatory response;
Polymorphism; Pyrrolidone carboxylic acid; 3D-structure.
PROBABLE: 1 23 PROBABLE: CYTOKINE AB.
CHAIN. 24 99 SMALL INDICIBLE CYTOKINE AB.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-95091716; PubMed=7999015;
Medline-95091716; PubMed=7999015;
Medling K.K., Knoke I.I., Klaudiny J.J., Wempe F.F., Wuttke W.W.,
Scheit K.K.,
"Porcine luteal cells express monocyte chemoattractant protein-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
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Best Local Similarity 62.7%; Pred. No. 1.6e-24;
Matches 47; Conservative 13; Mismatches 15; Indels
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01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
small inducible cytokine A8 precursor (CCL8) (Monocyte ct protein 2) (MCP-2) (Monocyte chemoattractant protein 2).
CCL8 OR SCYAR OR MCP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMALL INDUCIBLE CYTOKINE AB.
PYRROLIDONE CARBOXYLIC ACID.
BY SIMILARITY.
K -> Q.
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9D67976BB9422F2A CRC64;
                                                                                                                                                                                                                                                      GO; GG:0000009; F:chemokine activity; TAS.
GO; GG:0000009; F:signal transducer activity; TAS.
GO; GG:00006016; F:signal transducer activity; TAS.
GO; GG:00006116; F:cell-cell signaling; TAS.
GO; GO:00006915; P:cell-cell signaling; TAS.
GO; GO:0006817; P:exccytosis; TAS.
GO; GO:0000615; P:signal transduction; TAS.
InterPro; IPR000827; CC_chemkine_sml.
                                                                                                                           EMBL; X98865, CAA68168.1; ALT_INIT.
EMBL; Y18802, CAA71760.1; -.
EMBL; Y16645, CAA76341.1; -.
PIR; JCS295, JC5295.
PDB; LESR; 06-DEC-00.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 AA; 11246 MW;
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                                                                                                                                                                                                                              Genew; HGNC:10635; CCL8.
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SEQUENCE FROM N.A., AND SEQUENCE OF 17-98.
                                                                   MEDLINE=96235049; PubMed=8642349;
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Bartels J.,
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              REFERENCE OF THE FERENCE OF THE FERE
                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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(MCP-2): analysis by cDNA cloning and northern analysis.";
Biochem. Biophys. Res. Commun. 205:148-153(1994).
-!- FUNCTION: Chemotactic factor that attracts monocytes. This protein can bind heparin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 QPDSVSIPITCCFGLVNGKIPFKKLESYTRIINSQCPQBAVIFKTKADKEVCADPQQKWV
                                                                                                             -:- SUBUNIT: Monomer or homodimer; in equilibrium (By similarity).
-:- SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWART; SW00199; SCY; 1.
PROSITE; PS00472; SWALL CYTOKINES_CC; 1.
Cytokine; Chemotaxis; Signal; Heparin-binding; Inflammatory response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 OPDAINAPVICCYNFTNRKISVORLASYRRITSSKCPKEAVIFKTIVAKEICADPKOKWV
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15-JUL-1998 (Rel. 36, Last aquence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Small inducible cytokine Al3 precursor (CCLJ3) (Monocyte chemotactic
protein 4) (MCP-4) (Monocyte chemoattractant protein 4) (CK-beta-10)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
SMALL INDUCIBLE CYTOKINE A8.
PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.4%; Score 261; DB 1; Length 99; 60.0%; Pred. No. 1.1e-23; ive 16; Mismatches 14; Indels
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BY SIMILARITY.
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InterPro; IPR000837; CC chemkine sml.
InterPro; IPR001811; Chemokine_IL8.
Pfam; PF00048; IL8; 1.
SMART; SM00199; SCY; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pyrrolidone carboxylic acid.
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les 45; Conserv
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NEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schemen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schemen C.M., Ente F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Raba S.S., Loquellano W.A., Perers G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano W.A., Perers G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McZwan P.J., McZernan K.J., Malek J.A., Gunararne P.H.,

Rosak S.A., McZwan P.J., McZernan K.J., Malek J.A., Gunararne P.H.,

Rosak S.A., McZwan P.L., Soderspen E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Soderspen E.J., Lu X., Gibbs R.A.,

Raha S.Y., Madan A., Young A.C., Shevohenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Rodriguez A.C., Grimwood J., Schmutz J., Schmutz J., Schmutz J., Schmutz J., Schmutz J., Schmut
Uguccioni M., Loetscher P., Forssmann U., Dewald B., Li H., Lima S.H., Li, X Kraider B., Garotta G., Thelen M., Baggiolini M.; "Monocyte chemotactic protein 4 (MCP-4), a novel structural and functional analogue of MCP-3 and ectaxin.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIJUE=97741179; PubMed=9195948;
MEDIJUE=97741179; PubMed=9195948;
MEDIJUE=97741179; PubMed=9195948;
May an E., Reape T.J., Brawner M., Makwana J., Foley J.J.,
Schmidt D.B., Imburgia C., Macmulty D., Matthews J., O'Donnell K.,
O'Shannessy D., Scott M., Groot P.H.E., Macphee C.,
"Cloning, in vitro expression, and functional characterization of a novel human CC chemokine of the monocyte chemocractic protein (MCP) family (WCP-4) that binds and signals through the CC chemokine
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MEDLINE=97213770; PubMed=9060459;
Godiska R., Chantry D., Raport C.J., Schweickart V.L., Trong H.L.,
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MEDLINE=99160888; PubMed=10049733;
Hein H., Schluter C., Kulke R., Christophers E., Schroeder J.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Power C.A., Meyer A., Rison S.C.G., Guye-Coulin F., Wells T.N.C.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
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Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor 2B.";
J. Biol. Chem. 272:16404-16413(1997).
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                                                                                                                                                                                                                                                                   EXOGENOUS PATHOGONE.

- SUBCELLULAR LOCATION. Secreted.

- TISSUE SPECIFICITY: Widely expressed. Found in small intestine, thymus, colon, lung, trachea, stomach and lymph node. Low levels seen in the pulmonary arrery smooth muscle cells.

- INDUCTION: By interleukin-1 and TNF-alpha.

- INDUCTION: By interleukin-1 and ERS-30; METHOD-MALDI; RANGE=22-98.

- IN MASS SPECTROMETRY: MW=876; MW ERR=30; METHOD-MALDI; RANGE=22-98.

- IN MASS SPECTROMETRY: MW=876; MW ERR=30; METHOD-MALDI; RANGE=24-98.

- INDUCTION: MASS SPECTROMETRY: MW=876; MW ERR=30; METHOD-MALDI; RANGE=24-98.

- INDUCTION: MASS SPECTROMETRY: MW=876; MW ERR=30; METHOD-MALDI; RANGE=24-98.

- INDUCTION: MASS SPECTROMETRY: MM=876; MW ERR=30; METHOD-MALDI; RANGE=24-98.

- INDUCTION: MASS SPECTROMETRY: MM-876; MW ERR=30; METHOD-MALDI; RANGE=24-98.

- INDUCTION: MASS SPECTROMETRY: MM-876; MW ERR=30; METHOD-MALDI; RANGE=24-98.

- INDUCTION: MASS SPECTROMETRY: MM-876; MW ERR=30; METHOD-MALDI; RANGE=24-98.

- INDUCTION: MASS SPECTROMETRY: MM-876; MW ERR=30; METHOD-MALDI; RANGE=24-98.

- INDUCTION: MASS SPECTROMETRY: MM-876; MW ERR=30; METHOD-MALDI; RANGE=24-98.

- INDUCTION: MASS SPECTROMETRY: MM-876; MW ERR=30; METHOD-MALDI; RANGE=24-98.

- INDUCTION: MASS SPECTROMETRY: MM-876; MW ERR=30; METHOD-MALDI; RANGE=24-98.

- INDUCTION: MASS SPECTROMETRY: MM-876; MW ERR=30; METHOD-MALDI; RANGE=24-98.
                              Partels J.H., Schlueter C., Richter E., Noso N., Christophers E., Schroeder J.-M.; Schlueter C., Richter E., Noso N., Christophers E., Schroeder J.-M.; Achlueter C., Richter E., Noso N., Christophers E., Schroeder J.-M.; Achlueted C. T.-M.; Achlueter clouds and RT-PCR analysis."; Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases. -: FUNCTION: Chemotactic factor that attracts monocytes, lymphocytes. -: FUNCTION: Chemotactic factor that attracts monocytes, lymphocytes, -: FUNCTION: Chemotactic factor that attracts monocytes, lymphocytes, -: FUNCTION: Exceptors. Plays a role in the accumulation of Leukocytes at both sides of allergic and nonallergic inflammation. May be involved in the recruitment of monocytes into the arterial wall during the disease process of attherosclerosis. May play a role in the monocyte attraction in tissues chronically exposed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMALL INDUCIBLE CYTOKINE A13, LONG FOF SMALL INDUCTBLE CYTOKINE A13, SHORT FOF PYROLIDONE CARBOXYLIC ACID.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLONAC. ..) (POTENTIAL).
AHTIKT -> LTP (IN REF. 9).
12688DFCD308873 CRC64;
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GO, GO:0005615, C:extracellular space; TAS.
GO, GO:0008009; F:chemokine activity; TAS.
GO, GO:0005102; F:creceptor binding; TAS.
GO, GO:0006874; P:calcium ion homeostasis; TAS.
GO, GO:0006935; P:chemokaris; TAS.
GO; GO:0006935; P:chemokaris; TAS.
GO; GO:0006935; P:chemokaris; TAS.
GO; GO:0006935; P:chemokaris; TAS.
GO; GO:0006935; P:chemokaris; TAS.
InterPro; IPR000807; C.C.chemkine sml.
InterPro; IPR001811; Chemokine ILS.
InterPro; IPR008077; Fractalkine.
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SMART; SM00199; SCY; 1.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
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EMBL, AS9306, CA66650.1; --
EMBL, U59808, AAD09362.1; --
EMBL, AJ001634, CAA04888.1; --
EMBL, A7001634, CAA04888.1; --
EMBL, Z77650, CAB0111.1; --
HSSP, P51671; 1EOT.
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SEQUENCE OF 17-95 FROM N.A.
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DISÜLFID
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CARBOHYD
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                24 QPDALNVPSTCCFTFSSKKISLQRLKSY-VITTSRCPQKAVIFRTKLGKEICADFKEKWV
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MEDIATE=9193127; PubMed=2065676;

MEDIATE=9193127; PubMed=2065676;

Put W., Opdenakker G., Mantovani A.;

Production and identification of natural monocyte chemotactic

production and identification of natural monocyte chemotactic

the product from vitally infected murine fibroblasts. Relationship with
the product of the mouse competence (JE) gene.";

Eur. J. Biochem. 199:223-229(1991).

-i. FUNCTON: Chemotactic factor that attracts monocytes, but not
neutrophils.
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1010148; 0302D7;
10.0148r-1989 (Rel. 10, Created)
10.048r-1989 (Rel. 10, Last sequence update)
10.0CT-2003 (Rel. 42, Last annotation update)
Small inducible cytokine A2 precursor (CCL2) (Monocyte chemotactic protein 1) (MCP-1) (Monocyte chemoattractant protein-1) (Platelet-derived growth factor-inducible protein JE).

CCL2 OR SCYA2_OR MCP1 OR JE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -:- SUBCELLULAR LOCATION: Secreted.
-:- SUBCELLULAR LOCATION: Secreted.
-:- INDUCTION: By platelet-derived growth factor.
-:- POLYMORPHISM: The polymorphisms in strain SJL/J may be associa with severity of clinical symptoms of experimental allergic enceptablengwellits, an animal model of multiple sclerosis, and susceptibility to the monophasic remitting/nonrelapsing form of the disease.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kawahara R.S., Deuel T.F., "Plactor-inducible gene JE is a member of family of smail inducible genes related to platelet factor 4."; J. Blol. Chem. 264:679-682(1989).
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                                     62.6%; Score 253.5; DB 1
60.5%; Pred. No. 7.8e-23;
ive 16; Mismatches 13
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MEDLINE=89093129; PubMed=2910858;
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Query Match
Best Local Similarity bure
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                                                                                                                                                                                                                                                                                                                         61 QDSMDHLDKQTQTPKT
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completed: August 30, 2004, 17:05:15
ne : 25 secs
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                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Belongs to the intercrine beta (chemokine CC) family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Small inducible cytokine A8 precursor (CCL8) (Monocyte chemotactic
protein 2) (MCP-2) (Monocyte chemoattractant protein 2)
CCL8 OR SCYA8 OR MCP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bos taurus (Bovine).
Eukaryota, Metazos, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                  EMBL; AF065929; AAF15379.1; -.

EMBL; AF065930; AAF15379.1; -.

EMBL; AF065931; AAF15380.1; -.

EMBL; AF065931; AAF15381.1; -.

EMBL; AF065933; AAF15383.1; -.

REBL; A50009; AAF15383.1; -.

R PIR; S16226; S16226.

R PIR; S16226; S16226.

R GO; GO:000164; F:G-Protein-coupled receptor binding; IDA.

GO; GO:0005515; F:protein binding; IDA.

R GO; GO:0005515; F:protein binding; IDA.

R InterPro; IPR000827; CC_chemkine.sml.

R InterPro; IPR01811; Chemokine.ILB.
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                                                                                                                                                                                                                             EMBL; J04467; AAA37685.1; -.
EMBL; M19681; AAA37684.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ODSMDHLDK 69
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84 QTYIKNLDR 92
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AC 009171,
DT 5708_BOVIN
AC 009171,
DT 01-NOV-1995
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Cloning of the gene for bovine monocyte chemoattractant protein-2."; DNA Cell Biol, 13:1-8(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; S67954; AAD14005.1; --
EMBL; S67956; AAB29750.1; --
HSSP; PS1671; LEOT.
InterPro; IPR010811; Chemokine_IE8.
InterPro; IPR010811; Chemokine_IE8.
PF4m; PP00048; IL8; I.1.
SNART; SM00139; SCY; 1.
PROSITE; PS00472; SMALL CYTOKINES_CC; 1.
CROKINE; Chemotaxis; Signal; Heparin-binding; Inflammatory response;
                                                                                                               -!- SUBGNIT: Monomer or homodimer; in equilibrium (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
SMALL INDUCIBLE CYTOKINE A8.
PYRROLIDONE CARBOXYLIC ACID
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BY SIMILARITY.
BY SIMILARITY.
01974CDB3FF9119B CRC64;
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35 75
99 AA; 10900 MW;
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                                                                                         can bind heparin.
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Best Local Similarity
Matches 42; Conserv
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August 30, 2004, 16:59:28 ; Search time 115 Seconds (without alignments) 208.516 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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sparchea:*
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Seguence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Q9ttg3 equus cabal	Q865f3 macaca neme	Q7z7q8 homo sapien	Q8mkc8 equus cabal	Q865f4 macaca neme	Q8hyg0 macaca mula	Q8mit7 macaca mula	Q8hxz5 macaca mula	Q8cgm5 sigmodon hi	Q9ttg4 equus cabal	Q9z318 cavia porce	Q95md5 bos taurus	Q9tts6 bos taurus	Q9ttg2 equus cabal	Q9ttq1 equus cabal	
SUMMARIES			ID	Q9TTQ3	Q865F3	Q7Z7Q8	Q8MKC8	Q865F4	O8HXO0	Q8MIT7	Q8HXZ5	QBCGMS	Q9TTQ4	092318	•	O9TTS6	Q9TTQ2	OSTIGI	069560
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	дю (Query	Match	81.5	73.3	70.9	68.4	67.7	6.99	64.4	64.4	64.2	62.2	61.5	61.0	58.0	52.1	47.0	45.2
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ALIGNMENTS

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RESULT 1 29TTQ3	ID Q9TTQ3 PRELIMINARY; PRT; 99 AA.	AC Q9TTQ3;	01-MAY-2000 (TrEMBLrel, 13, Creat	(TrEMBLrel.	(TrEMBLrel. 24, Last	otein-	GN MCP-1.	OS Equus caballus (Horse).	Eukaryota; Metazoa;	Mammalia, Eutheria, Perissodactyla, Equidae, Equus.			Ī	-				RI "Cloning of equine chemokines eotaxin, monocyte chemoattractant			Vet. Immuno]. Immunopathol.	EMBL; AJ251189	HSSP; P13500; 1D	GO; GO:0005576; C:extracellular; IEA.	GO; GO:0008009;	DR GO; GO:0006955; P:immune response; IEA.	DR InterPro; IPR000827; CC chemkine sml.	DR InterPro; IPR001811; Chemokine I $\overline{ ext{L}}8$.	DR Pfam; PF00048; IL8; 1.	DR SMART; SM00199; SCY; 1.		KW Signal.	П	FT CHAIN 24 99 MONOCYTE CHEMOATTRACTANT PROTEIN-1.	SQ SEQUENCE 99 AA; 10790 MW; BA1448F79F3423D2 CRC64;
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Length 99;

DB 6;

81.5%; Score 330;

Query Match

0; Gaps

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1 QPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEGUENCE FROM N.A.
Takafuji V.A., Sharova L.V., Crisman M.V., Howard R.D.;
"Equus caballus monocyte chemoattractant protein-2 (mcp-2), complete
assignment to the C-C chemokine gene cluster on chromosome 17q11.2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monocyte chemoattractant protein-2.
Monocyte chemoattractant protein-2.
Bukaryota Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eŭkaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
                                                                                                                                                                                                                            Query Match
Best Local Similarity 72.0%; Pred. No. 6.4e-28;
Matches 54; Conservative 4; Mismatches 17; Indels
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                                                                                   Genomics 21:403-408(1994).
EMBL; X72309; CAB59723.1; -.
SEQUENCE 109 AA; 12356 MW; 69980669F0A2157D CRC64;
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01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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GO, GO:0005576; C:extracedlular; IEA.
GO, GO:0008009; F:chemokine activity; IEA.
GO, GO:0008555; P:immune response; IEA.
TherPro: IFR001811; Chemokine_IL8.
Pfam; PF00048; IL8; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9796;
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Q865F4;
01-JUN-2003
01-JUN-2003
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QBMKCB;
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Q865F4
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QSMKC8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 QPDGINTSTTCCYRFINKKIPKQRLESYRRITSSHCPREAVIFKTKLDKEICADPTQKWV 93
                                                                                                                                1 OPDAINAPVICCYNFINRKISVORLASYRRITSSKCPKEAVIFKTIVAKEICADPKOKWV 60
                                                                                                                                                                                                           83
                                                                                                                                                                              24 QPDAINSPUTCCYTFTGKKISSQRLGSYKRUTSSKCPKBAVIFKTILAKEICADPEQKWV
                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

Coleman G.D., Valii P.J.S., Clements J.E., Zink M.C.;

Coleman G.D., Valii P.J.S., Clements J.E., Zink M.C.;

Wacaca nemestrina (Pig-tailed macaque) monocyte chemoattractant protein-3 (MCP-3).";

Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AR206694, AA052735.1;

GO, GO:0005676; C:extracellular, IEA.

GO, GO:0005675; P:immune activity; IEA.

GO, GO:0006965; P:immune response; IEA.

InterPro; IPR001811; Cchemckine snl.

InterPro; IPR001811; Chemckine_IE8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=94375065; PubMed=7916328;
Opdenakker G.M.M.;
"The human MCP-3 gene (SCXA7): cloning, sequence analysis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . Match 73.3%; Score 297; DB 6; Length 109; Local Similarity 73.3%; Pred. No. 3.6e-29; les 55; Conservative 5; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monocyte chemoattractant protein-3.
Macaca nemestrina (Pig-tailed macaque).
Bukaryota, Metazoa, Chordata, Craniata; Vertebrata, Butelek
Mammalia; Butheria, Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                    78.7%; Pred. No. 2.5e-33; ative 9; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00048; IL8; 1.
SMART; SM01099, SCY; 1.
PROSITE; PS00472; SMALL CYTOKINES CC; 1.
SEQUENCE 109 AA; 12346 MW; D031826233EC461A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TremBlrel. 25, Created)
(TremBlrel. 25, Last sequence update)
(TremBlrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monocyte chemotactic protein-3. MCP-3.
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                                                                                                                                                                                                                                                                                                                                                84 QDAVKQLDKKAQTPK 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 QDSMDHLDKQTQTPK 75
                                                                                                                                                                                                                                                                                          61 QDSMDHLDKQTQTPK 75
                                                              59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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01-OCT-2003
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01-OCT-2003
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C72708
ID 7027
AC 0727
AC 0727
DT 01-0
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GN MCD-0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 OPDAINAPVICCYNFINRKISVORLASYRRIISSKCPKEAVIFKTIVAKEICADPKOKWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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SEQUENCE FROM N.A.

Coleman G.D., Clements J.E., Zink M.C.;

Macaca nemestrina (pig-tailed macague) MCP-2 (CC) chemokine.";

Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.

RMBL; AY206693; AA052734.1;

RGO; GO:0016576; C:extracellular; IEA.

RGO; GO:0016576; C:extracellular; IEA.

RGO; GO:0016576; C:emembrane; IEA.

RGO; GO:0016909; F:chemokine activity; IEA.

RITHERPO; IPR000181; CC.chemkine.sml.

RITHERPO; IPR001811; CC.chemkine.sml.

RITHERPO; IPR001811; Cmembxine.iEa.

REAT, PR00181; Cmembxine.iEa.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ChemoKine CCL8/MCP-2.
Macaca mulatta (Rhesus macaque).
Macaca milatta (Rhesus formata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
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BMBL, FAF495259; AAN76073.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.7%; Score 274; DB 6; Length 99, 62.7%; Pred. No. 2.4e-26; ive 14; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR01721; FRACTALKINE.
SMART; SM00199; SCY; 1.
PROSTIE: PS00472; SMALL.CYTOKINES CC; 1.
SEQUENCE: 99 AA; 11281 MW; 9D6797974A88B9BF CRC64;
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GO; GO:0005576; C:extracellular; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0008009; F:chemokine activity; IEA.
GO; GO:0008009; F:chemokine activity; IEA.
GO; GO:00069575; P:immune response; IEA.
InterPro; IPR000837; CC_chemkine sml.
InterPro; IPR001811; Chemokine IIB.
InterPro; IPR001811; Chemokine IIB.
PRINTS; PR01721; FRACTALKINE.
SMART; SM01721; FRACTALKINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99 AA.
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Best Local Similarity 62.7%,
Matches 47; Conservative
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47; Conserv
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Matches
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Q8HYQ0
DQ Q8HYQ0
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DT O1-O
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                   RATAR DESCRIPTION OF STAND OF 
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2 PDAINAPVICCYNFINRKISVQRLASYRRITSSKCPKBAVIFKTIVAKEICADPKQKWVQ 61
                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Chemokine CCL11/eotaxin.
Macaca mulatta (Rhesus macaque).
Eukaryotta; Metascoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;
Basu S., Schaefer T.M., Ghosh M., Fuller C.L., Reinhart T.A.;
"Comprehensive cloning and sequencing reveals evolutionary
conservation among all groups of rhesus macaque chemokines.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF449270; AANY6074.1;
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008009; F:chemokine activity; IEA.
GO; GO:0006955; P:immune response; IEA.
                                                                                                                                                                       Zhang L., Soares M.P., Guan Y., Sirotina-Meisher A.,
Matheravidathu S., Iliff S.A., Mudgett J.S., Springer M.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                Length 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Indels
                       01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Botaxin.
                                                                                                                                                                                                                                                                                                                                                                                                             64.4%; Score 261; DB 6; 63.5%; Pred. No. 9.8e-25;
97 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Mismatches
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                          Macaca mulatta (Rhesus macaque)
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83 DSMKYLDRKSPTPK 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 DSMDHLDKQTQTPK 75
                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 63.5
nes 47; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                               NCBI_TaxID=9544;
                                                                                                                                                                                                Daugherty B.L.;
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
CEMIT7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08HXZ5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
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1 OPDAINAPVTCCYNFTNRKISVORLASYRRITSSKCPKBAVIFKTIVAKEICADPKOKWV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 QPVSIS--TVCCFNVASRKISFQRLQSYRKITSSKCPQKAVIFKTKQAKKICADPKQKWV 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Lung;
Asano K., Matsubara H.,
Asano K., Yamaguchi K., Kanazawa M.;
Ishizaka A., Yamaguchi K., Kanazawa M.;
"Differential expression of CC chemokines in guinea pig lungs during an allergic inflammation.";
Submitted (MAY.1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB014340; BAA36456.1;
HSSP; PSI671; IROT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monocyte chemoattractant protein-3 (MCP-3).
Cavia porcellus (Guinea pig).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Hystricognathi, Caviidae, Cavia.
                                                                                                                                               "Cloning of equine chemokines eotaxin, monocyte chemoattractant protein (MCP)-1, MCP-2 and MCP-4, mRNA expression in tissues and induction by IL-4 in dermal fibroblasts."; Vet. Immunol. Immunopathol. 76:283-298(2000). EMBL; AJ291188; CAB61624-1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 62.2%; Score 252; DB 6; Length 100; Local Similarity 64.0%; Pred. No. 1.3e-23; les 48; Conservative 13; Mismatches 12; Indels
                                                                 SEQUENCE FROM N.A.
MEDLINE-21061912; PubMed=11044560;
Benarafa C., Cunningham F.M., Hamblin A.S., Horohov D.W.,
Collins M.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005576; C:extracellular; IEA.
GO; GO:0008009; F:chemokine activity; IEA.
GO; GO:0008055; P:immune response; IEA.
InterPro; IPR000827; CC chemkine sml.
PEam; PF00048; ILB; 1.
SMART; SM00199; SCY; 1.
SEQUENCE 97 AA; 11159 WW; E1B9Al7C165C2421 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN 24 100 ECTAXIN.
SEQUENCE 100 AA; 11247 MW; 11F08EC00E75D50B CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 AA.
                                                                                                                                                                                                                                                                            GO, GO:0005576; C:extracellular; IEA.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0008009; F:chemokine activity; IEA.
GO; GO:0006955; P:immune response; IEA.
InterPro; IPR000827; CC chemkine sml.
InterPro; IPR001811; Chemokine IEA.
InterPro; IPR001801; Fractalkine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                 PFam; PF00048; IL8; 1.
PRINTS; PR01721; FRACTALKINE.
SMART; SM00199; SCY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 ODSMDHLDKQTQTPK 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||:||:||:||
82 QDAMKYLDENSRTTK 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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100
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                           NCBI_TaxID=9796;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
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                                                                                                                                                                                                                                         2 PDAINAPVICCYNFINRKISVQRLASYRRIISSKCPKEAVIFKTIVAKEICADPKQKWVQ 61
                                                                                                                                                                                                                                                                     25 PDSV--ATTCCFTLTNKKIPLQRLESYRRIISGKCPQXAVIFKTKLAKDICADPKKKWVQ 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 OPDAINAPVICCYNFINRKISVORLASYRRITSSKCPKBAVIFKIIVAKEICADPKOKWV
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                                                                                                                                                                                                     2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sigmodon hispidus (Hispid cotton rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Sigmodontinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ectaxin precursor.
Equis caballus (Horse).
Eukaryotaballus (Abordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
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"Sigmodon hispidus cytokines, chemokines and interferons.";

"Sigmodon hispidus cytokines, chemokines and interferons.";

"Sigmodon hispidus cytokines, chemokines and interferons.";

"Submitted (OCT-2002) to the EMEL/GenBank/DDBJ databases.

"R EMBL; Al165951 AANS6566.1;

"R GO; GO:0008509; F:chemokine activity; IEA.

"R GO; GO:0008555; P:immune response; IEA.

"R GO; GO:0008555; P:immune response; IEA.

"InterPro; IPR001811; Chemokine sml.

InterPro; IPR001811; Chemokine_IEa.

"R Pfan; FR0048; ILB; 1.

"R SMART; SM0199; SCY; 1.

"R PARAT; SM0199; SCY; 1.

"R PRAT; SM0199; SCY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64.2%; Score 260; DB 11; Length 150; 63.2%; Pred. No. 2.1e-24; tive 11; Mismatches 17; Indels
                                                                                                                                                        Query Match

64.4%; Score 261; DB 6; Length 97;

Best Local Similarity 63.5%; Pred. No. 9.8e-25;

Matches 47; Conservative 14; Mismatches 11; Indels
                                                      Pfam; PF00048; IL8; 1.
SMART; SMO0199; SCY; 1.
PROSTIE; PS00472; SMALL CYTOKINES CC; 1.
SEQUENCE 97 AA; 10795 WW; EDOCD482880A47C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
             InterPro; IPR000827; CC_chemkine_sml.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monocyte chemoattractant protein-1.
                               IPR001811; Chemokine_IL8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85 OMYTKKWDONKARSET 100
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                                                                                                                                                                                                                                                                                                                                       62 DSMDHLDKQTQTPK 75
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DSMKYLDRKSPTPK 96
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Best Local Similarity
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01-JUN-2003
                                      InterPro;
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Matches

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RESULT 10

OBCGMS QBCGM5

RESULT 9 Q8CGM5

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Gaps

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Vogel B., Klinder A., Aust G.;
"Molecular cloning of bovine ectaxin mRNN.";
submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ132003; CAB61617.1;
HSSP; P51671; IEOT.
O GO, GO:0005576; C:extracellular; IEA.
GO, GO:0006595; F:chemokine activity; IEA.
GO, GO:0006955; P:immune response; IEA.
InterPro; IPR001811; Chemokine_ILB.
Fam; PF000489; IIS; 1.
SWART; SM00199; SCY; 1.
SEQUENCE 97 AA; 10965 MW; 9E65F23E1DDEB743 CRC64;
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              SURENTA
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                                                                                                                                                                                                                                              24 QPDGVNIS-TCCYK-RSQRIRVQRLESYTRITSSKCPWQAVIFKTRREICADPKQQWV
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01-DEC-2001 (TEMBLrel. 19, Last sequence update)
01-DEC-2003 (TEMBLrel. 24, Last sequence update)
01-UUN-2003 (TEMBLrel. 24, Last annotation update)
Chemoattractant protein 2 (Fragment).
Bos taurus (Bovine).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Cetartiodactyla; Ruminantia, Pecora, Bovoidea;
NCBL TaxID=9913;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Werling D.; "Role of chemokines in respiratory syncytial virus infection."; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF399641; AAK94451.1; -. HSSP; Q9Y258; 1G2S.
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56.0%; Pred. No. 5.6e-23;
tive 19; Mismatches 14; Indels
                                                                                                                   13; Indels
                                                Length
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01-WAY-2000 (TrEWBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                            Query Match
61.5%; Score 249; DB 11;
Best Local Similarity 63.2%; Pred. No. 3.1e-23;
Matches 48; Conservative 13; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 AA.
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GO; GO:0008009; F:chemokine activity; IEA.
GO:0006955; P:immune response; IEA.
InterPro; IPR000827; CC_chemkine_sml.
Figm.; PF00048; ILB,
FRMI; SM00199; SCY; I.
PROSITE; PS00472; SMALL_CYTOKINES_CC; 1.
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82 QDSMKYIDKKSKTPKS 97
                                                                                                                                                                                                                                                                                                                             61 ODSMDHLDKOTOTPKT 76
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nes 42; Conservative
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SEQUENCE FROM N.A.
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SEQUENCE
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O95MD5
O10 O95MD5
DT 01-DE
DT 01-DE
DT 01-DE
DE Chemo
OC Bwamma
OC Gwamma
OC
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                                                                                                                                                                                                                                24 QPASI--PTICCFNASKKKISIQRLQSYRKITSSKCPQKAVIFNTKQNKKICVDPQEKWV
                                                                                                                                                                            1 OPDAINAPVICCYNFINRKISVQRLASYRRIISSKCPKEAVIFKTIVAKEICADPKQKWV
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                                                                                        Gaps
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MEDINE-21061912;

MEDINE-2106192;

MEDINE-2106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Equus caballus (Horse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
                                                                                        ..
58.0%; Score 235; DB 6; Length 97
55.3%; Pred. No. 1.7e-21;
ive 20; Mismatches 12; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 24, Last annotation update)
Monocyte chemoattractant protein-2 precursor (Fragment).
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Pred. No. 1.4e-18;
9; Mismatches 11;
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BY SIMILARITY.
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82 QNAMEYINQKSQTLKS 97
         Query Match
Best Local Similarity 55.3†
Matches 42; Conservative
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es 38; Conserv
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Length 97;

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Q9TTQ1

D 09TTQ1

AC 09TTQ1

AC 09TTQ1;

D 09TTQ1;

D 10-MAY-2000 (TERMELeel. 13, Created)

DT 01-MAY-2000 (TERMELeel. 13, Last sequence update)

DT 01-MAY-2000 (TERMELeel. 13, Last sequence update)

DT 01-DUN-2003 (TERMELeel. 24, Last amontation update)

B MONCYPE chemcattractant protein-4 precursor (Fragment).

GN MCP-4.

OC Eduaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

NCB-TaxID-976;

RN MEDINE-2106-1912; PubMed=11044560;

RN MEDINE-2106-1912; PubMed=11044560;

RA Colling of equine chemokines ectaxin, monocyte chemoattractant

RT "Cloning of equine chemokines ectaxin, monocyte chemoattractant

RT induction by IL-4 in dermal iEbroblass ";

Vet. Immunol. Immunopathol. 76:283-298(2000).

DR EMB: AJS21191; CAB-1677.1; -

DR GO; GO:000555; C:extracellular; IBA.

DR GO; GO:000555; C:extracellular; IBA.

CO; GO:000555; C:extracellular; IBA.

DR GO; GO:000555; C:extracellular; IBA.

DR SWART; SMO0199; SCY: 1.

FT NOW TER 1 18 POTENTIAL.

FT NOW TER 75 75 MONOCYPE CHEMOATTRACTANT PROTEIN-4.

FT NOW TER 75 75 75 MONOCYPE CHEMOATTRACTANT PROTEIN-4.

FT NOW TER 75 75 75 MONOCYPE CHEMOATTRACTANT PROTEIN-4.

FT NOW TER 75 75 75 MONOCYPE CHEMOATTRACTANT PROTEIN-4.

FT NOW TER 75 75 75 MONOCYPE CHEMOATTRACTANT PROTEIN-4.

SQUENCE 75 AA; 8277 MM; 480A5267AC6A03E5 CRC64;

CHEMOATER 1; Mismatches 9; Indeels 1; Gaps 1;

Matches 9; Conservative 14; Mismatches 9; Indeels 1; Gaps 1;

Matches 9; Conservative 14; Mismatches 9; Indeels 1; Gaps 1;
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Search completed: August 30, 2004, 17:07:19 Job time : 119 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

score: 2,350-110 1: 1 cagccagatgcaatcaatgcaaacccaaac table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 1: 3470272 seqs, 21671516995 residues Imber of hits satisfying chosen parameters: 69
t score: 228 1 cagocagatgcaatcaatgcaaacccaaactccgaagact 22 1g table: IDENTITY_NUC Capop 10.0, Gapext 1.0 1470272 segs, 21671516995 residues number of hits satisfying chosen parameters: 6940544
ng table: IDENTITY_NUC Gapoxt 1.0 Gapop 10.0, Gapext 1.0 ned: 3470272 seqs, 21671516995 residues number of hits satisfying chosen parameters:
ned: 3470272 segs, 21671516995 residues number of hits satisfying chosen parameters:
number of hits satisfying chosen parameters:
Minimum DB seq length: 0 Maximum DB seq length: 200000000
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
gengabl::* gb ba::* gb ba::* gb on::* gb ov::* gb o
e :

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	71 Com 72 Nove 880 Synthy 880 Synthy 880 Synthy 880 Synthy 880 Synthy 880 Seq 74 Seq 74 Seq 74 Seq 74 Seq 74 Seq 74 Seq 75 Seq 76 Seq 76 Seq 77 Seq 77 Seq 78 Seq	DNA linear PAT 27-AUG-2002 ing primary pulmonary ata; Vertebrata; Buteleostomi; rhini; Hominidae; Homo. K., Ikeda, Y. and Inada, Y. ing primary pulmonary
SUMMARIES	BD102671 BD102671 BD137507 BD137507 BD177097 BD168034 BD177097 BD177097 BD5599 AXS98741 AXS98741 AXS98741 AXS977974 AXS98079 AXS77974 AXS98050 BD222014 AXS98970 BD222015 AXS98970 BD222015 AXS38970 BD222015 AXS38970 BD222015 AXS38970 BD222015 AXS38970 BD222015 AXS38971 BD222015 AXS38970 BD222015 AXS38970 BD222015 AXS38970 BD222015 AXS38970 BD222015 AXS38970 BD222015 AXS38970 BD222015 AXS38970 BD222015 AXS38970 BD222015 AXS38970 BD222015 AXS38971 BD232015 AXS38971 BD232015 AXS38971 BD232015 AXS38971 BD232015 AXS38971 BD232015 AXS38971 BD23320 BD083328 BD083328 BD088328 BD088328 BD088318 BD088318 BD188933 BD188933 BD088318 BD188933 BD18893 BD18893 BD18893 BD18893 BD18893 BD18893 BD18893 BD18893 BD18893 BD18893 BD18893 BD18893	228 bp nting or prevent 3245 Chordata; Crani Primates; Catar ssu,Y., Sueishi,
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sult No. Se	5 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	RESULT 1 BD102671 LDCUG DEFINITION C ACCESSION F VERSION F AUTHORS I
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarthini; Hominidae; Homo.

E 1 (bases 1 to 300)

E gashira, K., Takeshita, A., Koyanagi, M., Nakamuta, M. and Nishida, K. Noval hepatic disease agent

D Patent: WO 2030464-A. 2 18-APR-2002;

KENSUKE EGASHIRA, DAIICHI PHARMACEUTICAL CO LTD, AKIRA TAKESHITA, MASAMICHI KOYANAGI MAKOTO NAKAMUTA, KENICHI NISHIDA

OS Homo sapiens (human)

PD 18-APR-2002

PP 28-EBP-2001

PP 28-EBP-2001

PR 11-0CT-2000 UP 00P 310664

PI KENUKE EGASHIRA, AKIRA TAKESHITA, MASAMICHI KOYANAGI, MAKOTO PI
                                                                                                                                                                                                                                                                                                     1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTTATAACTTCACCAATAGGAAGATC
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                  /organism='Homo sapiens (human)' Location/Qualifiers
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                                                                                                                                                                               100.0%; Score 228; DB 6;
Similarity 100.0%; Pred. No. 7.2e-57;
28; Conservative 0; Mismatches 0;
                                                               1. .228
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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A61P11/00, C07K14/52, C07K16/24//C12N15/09, A61K37/02, C12N15/00
Preventive or remedy for pulmonary hypertension FH Key
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                                                                       WO 0189582-A/1
29-NOV-2001
25-MAY-2000
25-MAY-2000 JP 00P 161145
XENSUKE EGASHIRA, YOSHIKAZU YONEMITSU, KATSUO SUEISHI, YASUHIRO
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A61K48/00,A61K39/395,A61K38/17,A61K31/711,A61P91/00,A61P9/12
Composition for treating or preventing primary pulmonary CC
hypertension
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            TAKEDA CHEMICAL INDUSTRIES LTD, KENSUKE EGASHIRA, VOSHIKAZU YONEMITSU, KATSUO SUEISHI, YASUHIRO IKEDA, YOSHIYUKI INADA OS HOMO SUEISHI, YASUHIRO IKEDA, YOSHIYUKI INADA OS HOMO SUEISHI, YASUHIRO IKEDA, YOSHIYUKI INADA PN WO 0189582-A/1

PD 29-NOV-2001

PR 25-MAY-2001 WO 2011/P004381

PR 26-MAY-2001 DF 00P 161145

PI KENSUKE EGASHIRA, YOSHIKAZU YONEMITSU, KATSUO SUEISHI, YASUI PI IKEDA,

PI YOSHIYUKI INADA

PC AGIKARAPOO, AGIKAS9/395, AGIKASB/17, AGIKA31/711, AGIP11/00, AGIP

C COMPOSITION for treating or preventing primary pulmonary
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Location/Qualifiers
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Preventive or remedy for pulmonary hypertension.
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SOURCE
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                         FEATURES
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PAT 17-JAN-2003

linear

DNA

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1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC 60
                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                              organism='Homo sapiens (human)'.
                                                                                                                                                                                                                                                                                  Length 300;
                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 228; DB 6; Best Local Similarity 100.0%; Pred. No. 7.3e-57; Matches 228; Conservative 0; Mismatches 0;
Novel hepatic disease agent
Key Location/Qualifiers
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Db 70 CAG	CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC 129	BT007880 LOCUS	BT007880
Oy 61 TCA(DEFINITION	Synthetic construmRNA, partial cd
130	TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGAGTGTCCCAAAGAAGCT 189	ACCESSION VERSION KRYWORDS	BT007880 BT007880.1 GI:30 FI:1 CDNA.
OY 121 GTG	GEGATUTICAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGGAGTGGGTT 249	SOURCE	synthetic constru synthetic constru artificial sequen
Qy 181 CAG Db 250 CAG	CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 228 	REFERENCE AUTHORS	
		TITLE	Phelan, M. and Far Cloning of human
	BD177097 Prophylactic and/or remedy for vascular restenosis.	JOURNAL REFERENCE AUTHORS	vector Unpublished 2 (bases 1 to 3 Kalnine, N., Chen Koundince M. Ren
ACCESSION BD177 VERSION BD177 KEYWORDS JP 20 SOURCE HOMO	BD177097 BD177097.1 GI:30014357 YP 2002284698-A/2. Homo sapiens (human)	TITLE JOURNAL	Phelan, W. and Far Direct Submission Submitted (13-MA)
	Homo sapiens Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	COMMENT	This CDS clone i
REFERENCE 1 (b AUTHORS Egash TITLE Proph JOURNAL Paten	. vascular res ocr-2002;		Harvard Institut forms: with and tag). The CDS ha cloning system b
	JKE EGASHIRA,DAIICHI PHARMACEUTICAL CO LTD Homo sapiens (human) JP 2002284698-A/2		Vector. Addition and before 'ATG' last codon and b
PD PF	03-0CT-2002 23-MAR-2001 JP 2001085073 KENSUKE EGASHIRA,AKIRA TAKESHITA	FEATURES source	,
PC A61K4	15/00, A61K31/711, A61K35/76, A61K38/00, A61K39/395, A61K39/395, PC		/mol_ty /db_xre
A61K PC Proph	A61K48/00, PC A61P9/10,A61P9/10//C12N15/09,A61K37/02,C12N15/00 CC Prophylactic and/or remedy for vascular restenosis FH Key Location/Oualifiers		/clone= /clone collect
ET FEATURES	<pre>source</pre>	CDS	/lab_ho /note=" 1, .>30
source	1300 /organism="Homo sapiens" /nol type="genomic DNA" /Ab	·	/note=" /codon /trans] /produc
ORIGIN			/protei /db_xre
Query Match Best Local Similarity Matches 228; Conser	100.0%; Score 22%; DB 6; Length 300; llarity 100.0%; Pred. No. 7.3e-57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	ORIGIN	/transi VQRLASY
Cy 1 CAC Db 70 CAC	CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC 60 	Query Match Best Local Matches 22	cch al Similarity 10 228; Conservativ
Oy 61 TCA Db 130 TCA	TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAAGTGTCCCAAAGAAGCT 120 	& 9a	1 CAGCCAGATGCAAT
Oy 121 GTC	GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT 180	à	
Db 190 GTC	GIGATCTTCRAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT 249	d _O	130 TCAGTGCAGAGGCT
	181 CAGGATTCCAIGGACCACCTGGACACACACACTCCGAAGACT 228		121 GTGATCTTCAAGAC
Db 250 CAC	GGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 297	g 8	

RESULT 5

Jacky-2003) BD Biosciences Clontech, 1020 East Meadow Jacky-2003) BD Biosciences Clontech, 1020 East Meadow Jacky-2003) BD Biosciences Clontech and the clones generated by BD Biosciences Clontech and the clones generated by BD Biosciences Clontech and the and without stop-coden (to allow fusion with C-terminal sequences in the clone 'ACC' after Sall site ATG' to provide Kozak consensus sequence; 'GG' after and before HindIII site to maintain reading frame. Tatton/Qualifiers

and before HindIII site to maintain reading frame. Cation/Qualifiers

and synthetic construct" a start=1
sl_table=11
sl_table=11
cot="Home sapiens chemokine (G-C motif) ligand 2"
ein id="AaP36552.1"
ref="GI:30584591"
ref="3130584591"
slation="WKSAALCLIALIAATFIPQGLAQPDAINAPVTCCYNFTNRKIS
SYRRITSSKCPKEAVIFKTIVAKEICADPKQWVQDSMDHLDKQTQTPKTL" n,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., aphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y., 300) nn,X., Rolfs,A., Halleck,A., Hines,L., Eisenstein,S., apphael,J., Moreira,D., Kelley,T., LaBaer,J., Lin,Y., 'armer,A. ö ACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT 180 300 bp mRNA linear SYN 13-MAY-2003 ruct Homo sapiens chemokine (C-C motif) ligand 2 ARCAATGCCCCAGTCACCTGCTGTATAACTTCACCAATAGGAAGGTC 60 TCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCCAAAGAGGT 120 : lib="BD Creator(TM) CDS Library derived from MGC trion" armer,A. n full-length CDSs in BD Creator(TM) System Donor 0; Gaps 00.0%; Score 228; DB 12; Length 300; 00.0%; Pred. No. 7.3e-57; ve 0; Mismatches 0; Indels 0 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 228 lost="DH5alpha T1 resistant" "Vector: pDNR-Dual" "Mutations: 299:Stop->Leu" Ype="mRNA" ef="taxon:32630" :="GH00237L1.0" 30584598 ences. 181 (ઠ

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YAMADA

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Yamagishi,J., Matsuo,T., Fukui,J. and Yamada,M.
PRODUCTION OF MONOCYTE CHEMOTACTIC FACTOR POLYPEPTIDE AND MICROBIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lyamichev, V., Skrzpczynski, Z., Allawi, H.T., Wayland, S.R., Takova, T. and Neri, B.P.
Charge tags and separation of nucleic acid molecules
Patent: WO 02063030-A 72 15-AUG-2002;
THIRD WAVE TECHNOLOGIES, INC. (US)
                                                                                                                                                                                             Č12P21/02,C12N1/21//C12N15/12,(C12P21/02,C12R1:19),(C12N1/21,C12R1:19);
C12R1:19);
strandedness: Double;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 TCAGTGCAGAGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 GTGATCTTCAAGACCATGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CAGCCAGATGCAATGAATGCCCCAGTCACCTGCTTATAACTTCACCAATAGGAAGATC
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                                                                                                                                                                                                                                                                                                                                                                         /product='monocyte chemotactic factor'
40. .270
                                                                                                                                                                                                                                                                                                                                                                                                                          /product='monocyte chemotactic factor'
                                 STRAIN PRODUCING THE POLYPEPTIDE
Patent: JP 1993560987-A 3 12-OCT-1993;
Patent: JP 1993260987-A 3 12-OCT-1993;
PD 12-OCT-1993
PD 12-OCT-1993
PF 28-APR-1992 JP 1992136213
PR 99-MAY-1991 JP 11P 135950
PI YAMAGISHI JUNICHI, MATSUO TOKUYUKI, FUKUI JUICHI, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 554;
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100.0%; Score 228; DB 6;
Best Local Similarity 100.0%; Pred. No. 7.4e-57;
Matches 228; Conservative 0; Mismatches 0;
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Sequence 72 from Patent WO02063030.
AX698741
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1. 554
Acgains="Escherichia oc/mol_type="genomic RNA"
/db_xref="taxon:562"
                                                                                                                                                                                                                                                                                                                                       1. .39
22. .29
40. .267
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hypothetical: No;
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   AUTHORS
TITLE
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                                                                                            THOSE STATEMENT CONSTRUCT

THOSE STATEMENT TO A18)

THOSE STATEMENT OF MACHOLIC FACTOR POLYBEPTIDE AND MICROBIAL STRAIN PRODUCTION OF MONOCYTE CHEMOTACTIC FACTOR POLYBEPTIDE AND MICROBIAL PRODUCTION OF MONOCYTE CHEMOTACTIC FACTOR POLYBEPTIDE AND MICROBIAL STRAIN PRODUCTION OF MONOCYTE CHEMOTACTIC FACTOR POLYBEPTIDE AND MICROBIAL PARAMACEUT CO LTD

T OS ATLIFICIAL General Sequence: CT OF ATLIFICIAL SEQUENCE: CT ON APP 1993260407
                                                                                          29-SEP-1997
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Enterobacteriaceae, Escherichia.
1 (bases 1 to 554)
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09-WAY-1991 JP 91P 135950
YAWAGISHI JUNICHI, MATSUO TOKUYUKI, FUKUI JUICHI, PI
                                                                                          PAT
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;
250 CAGGATTCCATGGACCACCTGGACAAGCAAACCCCAAACTCCGAAGACT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 228
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100.0%; Pred. No. 7.4e-57;
ive 0; Mismatches 0;
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                        DNA
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strandedness: Single;
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hypothetical: No;
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JP 1993260987-A/3.
Escherichia coli
Escherichia coli
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Matches 228; Conservative
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TITLE
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121 GIGAICTICAAGACCAITGIGGCCAAGGAGAICTGIGCIGACCCCAAGCAGAAGIGGGIT 180
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 cadecadarida arcearde ce centra e contra e c
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                                                                     1 (bases 1 to 725)
Cocks B.G., Stuart, S.G. and Seilhamer, J.J.
Compositions for the detection of blood cell
response gene expression
Patent: US 6607879-A 1344 19-AUG-2003;
Location/Qualifiers
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Patent: WO 03038129-A 58 08-MAY-2003;
Ortho-Clinical Diagnostics, Inc. (US)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db xref="taxon:9606"
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Sequence 58 from Patent WO03038129.
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/organism="unknown"
/mol_type="genomic DNA"
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Unknown.
Unclassified.
I (bases 1 to 725)
Garzino-modulating effects of chemokines in DNA vaccination
Immuno-modulating effects of chemokines in DNA vaccination
Patent: US 6569418-A 3 27-MAY-2003;
Location/Qualifiers
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Similarity 100.0%; Pred. No. 7.5e-57;
8; Conservative 0; Mismatches 0;
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/mol_type="unassigned RNA"
/db_xref="taxon:32630"
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Sequence 3 from patent US 6569418.
AR337874
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AR380799
AR380799.1 GI:40088433
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 739)
Yoshimura, T. and Leonard, E.J.
                                                                                                                                                                                                                                                                         Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Location/Qualifiers
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303 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 350
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Adv. Exp. Med. Biol. 305, 47-56 (1991)
92095166
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                                                                                                                           DNA
                                                                                                                       739 bp 1
Sequence 96 from Patent WO02081745.
AX577974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="mRNA"
                                                                                                                                                                                       AX577974.1 GI:27647182
                                                                                                                                                                                                                                 Homo sapiens (human)
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                                                                                                                                                    HSMCP1 725 bp mRNA linear PRI 03-APR-1995
H.sapiens mRNA for monocyte chemoattractant protein 1 (MCP-1).
X14768
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VQRLASYRRITSSKCPKEANI FKTIVAKEICAD PROKWWQD SMDHLDKQTQTPFRT"
                                                                                                                                                                                                                                                                                                                                                                                                                  Human monocyte chemoattractant protein-1 (MCP-1). Full-length cDNA cloning, expression in mitcgen-stimulated blood mononuclear leukocytes, and sequence similarity to mouse competence gene JE PEBS Lett. 244 (2), 487-493 (1989)
2465924
ZAPII.
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Yoshimura, T., Yuhki, N., Moore, S.K., Appella, E., Lerman, M.I. and
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/note-"pot. N-linked glycosylation site"
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ilarity 100.0%; Pred. No. 7.5e-57;
Conservative 0; Mismatches 0;
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162. .170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_line="Ul05MG" /cell_type="glioma cells" /clone_lib="lambda" /clone_lib="lambda"
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1. 725. wailfiers
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7. mol_type="mRNA"
7. db_xref="taxon:9606"
7. cell_line="H1706.06"
                                                                                                                                                                                                                                                     monocyte chemoattractant protein 1.
Homo sapiens (human)
Homo sapiens
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/note="polyA site"
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121 GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAGTGGGTT 180
139 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGAAAGATC 198
                                                                                                                         199 readracadadacreacadacraragadadareaceadeadacrereceaadadacr
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258 120

259 GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT 318

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181 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 228 319 CAGGATICCAIGGACCACCIGGACAAGCAAACTCCGAAGACT

Search completed: August 31, 2004, 03:22:47 Job time : 1394 secs

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54. 353

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                                                      'gene="monocyte chemoattractant protein-1, MCP-1"
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100.0%; Score 228; DB 9; Length 739;
Best Local Similarity 100.0%; Pred. No. 7.5e-57;
Matches 228; Conservative 0; Mismatches 0; Indels
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1. .739
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linear PAT 30-SEP-1994 unidentified
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unidassified.
1 (bases 1 to 741)
Caput, D., Ferrara, P., Miloux, B., Minty, A. and Vita, N.
Protein with cytokine activity, recombinant DNA, expression vector and hosts for obtaining it
Patent: EP 0488900-A 25 03-JUN-1992;
ELF SANOFI mRNA 741 bp A17786 MCP-1 mRNA. A17786 A17786.1 GI:641144 RESULT 15
A17786
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VERSION
KEYWOEDS
SOURCE
ORGANISM REFERENCE AUTHORS TITLE JOURNAL

FEATURES

gene CDS

Location/Qualifiers

1. 741

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1. 741

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1. 741

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ORIGIN

Gaps ; 0 Query Match 100.0%; Score 228; DB 6; Length 741; Best Local Similarity 100.0%; Pred. No. 7.5e-57; Matches 228; Conservative 0; Mismatches 0; Indels (

; 0

1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGTTATAACTTCACCAATAGGAAGATC 60

(oideu) Arrola agod eirii

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

August 30, 2004, 16:49:10 ; Search time 236 Seconds (without alignments) 4104.191 Million cell updates/sec Run on:

07330446 228 1 cagccagatgcaatcaatgc.....aaacccaaactccgaagact 228 Title: Perfect score: Sequence:

Scoring table: IDENTITY_NUC Gapop 10.0, Gapext 1.0

Total number of hits satisfying chosen parameters: 3373863 seqs, 2124099041 residues Searched:

6747726

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_290an04:*

1: geneseqn1908:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001as:*

6: geneseqn2001s:*

7: geneseqn2003as:*

8: geneseqn2003as:*

10: geneseqn2003as:* Database :

Pred, No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Aba02497 Human mon	Abl60575 Human mon	Acc42732 Monocyte		Abs68800 Human mon	Aag85370 Chemoattr	Aax80631 Monocyte	Aad58817 Human mon	Add18494 Human pro	Ade84839 Farnesyl	Aan91337 DNA which	Aav10341 cDNA enco	Н	Abz34738 Coding se	. Aaa34899 Human ade	Aaf21021 Human low	Abz96715 Human nuc	Add14996 Human mon	\leftarrow	3 Human	Aaz61117 DNA encod	— œ	Aaz61119 DNA encod
SUPERMIES	ID	ABA02497	ABL60575	ACC42732	ABV97697	ABS68800	AAQ85370	AAX80631	AAD58817	ADD18494	ADE84839	AAN91337	AAV10341	ABV78071	ABZ34738	AAA34899	AAF21021	ABZ96715	ADD14996	AAZ33515	ABX63583	AAZ61117	AAZ61118	AAZ61119
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Aav34249 Human sec	Acd08120 cDNA enco	Aav34248 Human sec	Acd08119 cDNA enco	Aag05625 Human MCF	Matu	Aav86200 EST clone	EST	Aag30749 MCF (DraI	Abv96715 Human pan	Aag30745 MCF (SS)	Aaa74882 Human che	Aag30748 pHMCF7. 3	Aat48092 Monocyte	Aaq30746 MCF (DS)	Aaa44418 Human sec	Aav86195 EST clone	Abl60574 Human mon	Acc42733 Monocyte	Aba02498 Human mut	Aax24805 Human mon	Aav88315 EST clone
AAV34249	ACD08120	AAV34248	ACD08119 .	AAQ05625	AAT03528	AAV86200	AAV86197	AAQ30749		AAQ30745	AAA74882	AAQ30748		AAQ30746	AAA4418	AAV86195	ABL60574	ACC42733	ABA02498	AAX24805	AAV88315
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99.8	8.6	ω.	8.6	9.66	99.3	99.3	89.3	99.3	99.3	99.3	99.3	99. ₃	98.6	97.2	96.7	2	-	90.0	89.5		84.7
227.6	227.6	227.6	227.6	227.2	226.4	226.4	226.4	226.4	226.4	226.4	226.4	226.4	224.8	221.6	220.4	211.2	205.2	205.2	204	196	193.2
24						30		32	33	34	35	36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

RESU	RESULT 1 ABA02497
ПX	ABA02497 standard; DNA; 228 BP.
S S	ABA02497;
(日)	26-MAR-2002 (first entry)
E E	Human monocyte chemoattractant protein-1 (MCP-1) DNA.
{ & & \$	Human; monocyte chemoattractant protein-1; MCP-1; C-C chemokine family; pulmonary hypertension; primary; hypotensive; gene; ds.
so	Homo sapiens.
きまり	Poo.
# # # # # # F # # # # #	CDS 1.228 /*tag= a /partial /product="Human MCP-1" /note="No start or stop codon given in the
	<pre>mutation replace(325, GG) /*tag= b //note= "The sequence encoding the 7ND-MCP-1 mutant (ABA02498) contains a 24 bp deletion relative to this sequence"</pre>
X E S	WO200189582-A1.
₹ 8	29-NOV-2001.
Z E	25-MAY-2001; 2001WO-JP004381.
1E	26-MAY-2000; 2000JP-00161145.
48 B B	(TAKE) TAKEDA CHEM IND LTD. (EGAS/) EGASHIRA K.
Z II X	Egashira K, Yonemitsu Y, Sueishi K, Ikeda Y, Inada Y;
888	WPI; 2002-083059/11. P-PSDB; AAM53048.
5 E E	Preventives and remedies for pulmonary hypertension containing mutant of MCP-1 antagonistic inhibitory type or its salt, encoded DNA or

Disclosure;

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Query Match

121

181

181

ABL60575

RESULT ABL6057

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Gaps

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129 120 189 180 249

228

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function inhibitor as the active ingredient. The MCP-1 function inhibitors are useful in treating and preventing hepatic diseases such as liver fibrosis or liver cirrhosis. The present sequence represents a human MCP-1 related DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a method for preventing or treating organ transplant rejection. The method comprises preventing arteriosclerosis or endothelial thickening in blood vessel autograft or allograft, post-transplant, using an agent which inhibits the function of monocyte chemotactic protein ! (MCP-1). The present sequence was used to illustrate the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, immunosuppressive, organ transplant rejection, arteriosclerosis, endothelial thickening, monocyte chemotactic protein 1; MCP-1; ds.
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                                                                                                                                                                                                                                                                                                                              61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCCAAAGAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGCCAGATGCAATGCCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
                                                                                                                                                                                                                                                                                70 cagccagargcaarcaargccccagrcaccrgcrgrraraacrrcaccaaragaagarc
                                                                                                                                                                                                                                                                                                                                                     GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monocyte chemotactic protein 1, MCP-1, related sequence, SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 297
                                                                                                                                                       Length 300;
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                                                                                                                                                                                                Indels
                                                                                                           Sequence 300 BP; 83 A; 88 C; 68 G; 61 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 300 BP; 83 A; 88 C; 68 G; 61 T; 0 U; 0 Other;
                                                                                                                                                     Score 228; DB 6;
Pred. No. 3.8e-62;
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                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP
                                                                                                                                                  100.0%;
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                                                                                                                                                                                                Matches 228; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EGAS/) EGASHIRA K.
                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAY-2003
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                                                                                                                                                       Query Match
Best Local 8
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                                                                                  The invention relates to preventives and remedies for pulmonary hypertension, comprising an antegonistic inhibitory mutant of monocyte chemoattractant protein-1 (MCP-1), DNA encoding the mutant MCP-1, or a neutralising antibody against MCP-1. MCP-1 is a member of the C-C and expension family. The preventives and remedies have hypotensive activity and can be used in the prevention and treatment of pulmonary hypertension particularly pulmonary primary hypertension. The present sequence represents DNA encoding wild-type human MCP-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treating hepatic diseases comprise a monocyte chemoattractant
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                                                                                                                                                                                                                                                                                                                                                                                                                   CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT
                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGGATTCCATGGACCACCTGGACAAGCAAACCCCAAACTCCGAAGACT 228
                                                                                                                                                                                                                                                                                                                              DB 6; Length 228;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT
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                                                                                                                                                                                                                                                                                   Sequence 228 BP; 71 A; 62 C; 53 G; 42 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                            100.0%; Score 228; DB 6;
100.0%; Pred. No. 3.4e-62;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human monocyte chemoattractant protein-1 (MCP-1)
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                                             Page 32; 39pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 10; 18pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
ses 228; Conservative
    neutralization antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-394437/42.
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Egashira K,

Agents for

18-APR-2002

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WO200263030-AZ. Homo sapiens 20-NOV-2002 15-AUG-2002 61 181 ABS68800; Neri BP; AESULT 5 ABS68800 9 Q ò g à a 8 쉽 o; The invention relates to an isolated polynucleotide (I) comprising: (a) any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b) complements of (a); (d) sequences consisting of at least 20 contiguous residues of (a); (d) sequences that hybridize to (a), under moderately stringent conditions; (e) sequences having at least 75% or 90% identity to (a); or (f) degenerate variants of (a). Polypeptides (ABP66596-ABP66637) encoded by (I) and oligonucleotide can be used to detect cancer in a patient and compositions comprising polypeptides, polynucleotides, antibodies, fusion proceins, T cell populations and antigen presenting cells expressing the polypeptide are useful in treating pancreatic cancer 120 249 130 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGAAGCT 189 GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT 180 9 New isolated polynucleotide and pancreatic tumor polypeptides, useful f diagnosing, preventing and/or treating cancer, particularly pancreatic 190 GIGAICTICAAGACCATIGIGGCCAAGAGAGATCIGIGCIGACCCCAAGAGAGAGGIT CAGCCAGATGCAATCAATGCCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC cadocadaridaarideceedagreactidergranaactreaceariadeaac TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT Gaps Jiang Y; therapy; vaccine; immunostimulant; .. 0 228 Claim 1; SEQ ID NO 3105; 300pp + Sequence Listing; English. CAGGATTCCATGGACCACCTGGACAAGCAAACTCCGAAAGACT CAGGATTCCATGGACCACCTGGACAAGCAAACCCCAAACTCCGAAGACT Hepler WT, Indels Human pancreatic cancer expressed cDNA SEQ ID NO 3105. No. 3.8e-62; Persing DH, Pred. No. 3.8 Mismatches 100.08; Lodes MJ, BP. RESULT 4
ABV97697
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ABV97697;
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S0-JAN-2001; 2001US-026568P.
PR 31-JAN-2001; 2001US-026568P.
PR 31-JAN-2001; 2001US-026568P.
PR 31-JAN-2001; 2001US-026568P.
PR 31-JAN-2001; 2001US-026568P.
PR 21-MAR-2001; 2001US-028586P.
PR 21-MAR-2001; 2001US-0333626P.
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CORI-) CORICA CORP.
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New isolated polynucleotide and diagnosing, preventing and/or tip
PT cancer.
XX
CC The invention relates to an iso
CC Tesidues of (a); (b) sequences
CC Tesidues of (a); (c) sequences
CC Tesidues of (a); (d) Conservative Similarity Best Local Sim: Matches 228; H 20 61 121 181

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and stimulating an immune response. The polynucleotides can be used as probes or primers for nucleic acid hybridisation, in the design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in the tumour cells, in vaccines and for gene therapy. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      284 GTGATCTTCAAGACCATTGTGGCCCAAGGAGATCTGTGCTGACCCCAAGGAGAAGTGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCCAAAGAAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCCAGCAGCAAGTGTCCCCAAAGAAGCT
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                                                                                                                                                                                                                                                                                                                                                                                 Length 475;
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100.0%; Pred. No. 4.6e-62;
ive 0; Mismatches 0;
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Best Local Similarity 100.'
Matches 228; Conservative
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Query Match Best Loc Matches 70 61 130 121 190 181

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Garzino-Demo A;
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54. .353
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07. .712
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/product= '
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Matches 228; Conservative
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molecules, the method provides an absolute readout of the partition of products from substrates (i.e. provides a 100% separation). Through the use of multiple positively charged adducts, synthetic molecules can be constructed with sufficient modification due to the fact that the normally negatively charged strand is made nearly neutral. It is also possible to distinguish between a enzymatically or thermally degraded DNA fragments due to the absence or presence of 3'phosphate. ABS68740-ABS68813 represent coding sequences and primers used in the method of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Purified heparanases, prepared under reducing conditions and activated with transglutaminase, are given in AAR70786-805. Most are prepared by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GUGAUCTUCAAGACCAUGUGGCCAAGGAGAACUGUGCCCGAAGCCAAGCAGAGGGGUU
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                                                                                                                                                                                                                                                                                     Sequence 647 BP; 180 A; 146 C; 121 G; 0 T; 200 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                       %; Score 228; DB 6;
; Pred. No. 5.2e-62;
42; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                             100.0%;
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93US-00136117.
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                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 81.6%;
nes 186; Conservative 4
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(first entry)
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29-AUG-1995
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AAQ85370;

AAQ85370 RESULT

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182
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reverse transcription of mRNA from activated human leukocytes, then clouning of the cDNA into pVL1392 bacultovirus vector, and expression in Sf9 cells in the presence of reduced glutathione and dithiothreitol. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 GIGATCTICAAGACCATIGIGGCCAAGGAGAICTGIGCTGACCCCAAGCAGAAGIGGGIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT
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                                                                                                                                                                                                                                                 Length 725;
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label= Monocyte_chemoattractant_protein_1
function= "chemotactic for monocytes"
                                                                                                                                                                            Sequence 725 BP; 208 A; 171 C; 126 G; 220 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                         100.0%; Score 228; DB 2;
100.0%; Pred. No. 5.4e-62;
ive 0; Mismatches 0;
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15-JAN-2004
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                                                                                                                                                                    (MCP-1) DNA
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                                                           The present sequence encodes monocyte chemoattractant protein-1. The efficacy of a vaccine is enhanced by combining it with one or more chemokines. This can be used to enhance humoral or cell-imediated immune response. The purified nucleotide sequence encoding the chemokine, fragments, derivatives, analogues, or truncation isoforms are expressed in a coordinated manner upon introduction in a suitable cell. These sequence are operably linked to one or more gene regulatory elements. The mucleic acid may have deletional, insertional, or substitutional mutations. They are referred as DNA vaccines and are administered by constructing an expression plasmid vector either directly or indirectly. The chemokine gene is isolated by PCR, which can be used to amplify the desired sequence in a genomic or cDNA library. The vaccines can be used to treat microbial diseases especially HIV
                                                                                                                                                                                                                                                                                            TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCCAAAGAAGCT 120
                                                                                                                                                                                                                                                                                                                                               242
                                                                                                                                                                                                                                                                                                                                                                   GIGAICTICAAGACCATIGIGGCCAAGGAGAICTGIGCTGACCCCAAGCAGAAGTGGGTI 180
                                                                                                                                                                                                                                                                                                                                                                             Human; immune response; vaccine; macrophage derived chemokine; MDC; anti-HIV; virucide; immunostimulant; monocyte chemoattractant protein 1;
                                                                                                                                                                                                                                                                               1 CAGCCAGATGCAATGCCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
                                                                                                                                                                                                                                                                                                                                              TCAGTGCAGAGCTCGCGAGCTATAGAAGAATCACCAGCAGCAGTGTCCCAAAGAAGCT
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                                                                                                                                                                                                                                   100.0%; Score 228; DB 2; Length 725; 100.0%; Pred. No. 5.4e-62; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                 Seguence 725 BP; 208 A; 171 C; 126 G; 220 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human monocyte chemoattractant protein 1 (MCP-1) DNA.
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                     of enhancing vaccine efficacy
                                           Claim 22; Page 65-66; 134pp; English
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02-MAR-2000; 2000US-0186416P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD58817 standard; DNA; 725
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                                                                                                                                                                                                                                                             228; Conservative
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                                                                                                                                                                                                                                                  Similarity
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  P-PSDB; AAY26176
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Best Local (
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prostate tissue; cancer diagnostic; cancer marker; prostate cancer; PCA; male cancer-related death; serum biomarker; tissue biomarker; cytostatic; gene therapy; prostate biopsy tissue; AMACR; alpha-methylacyl-coenzyme A racemase; diagnosing cancer; cell growth; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                          The invention relates to a method for improving immune response to an HIV antigen. The method involves administering to the subject a composition which comprises: an isolated HIV antigen (e.g., gpl20) or gpl80) against which an immune response is desired in subject, chemokine, such as macrophage derived chemokine (MDC) and a carrier. The method is useful for improving subject's immune response to HIV antigen (e.g., gpl20 or gpl80). The invention is useful for enhancing the efficacy of immune response against the antigen in a subject. The invention is useful as
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administering composition gp160, a macrophage derived
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 228; DB 9; Length 725;
Best Local Similarity 100.0%; Pred. No. 5.4e-62;
Matches 228; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 725 BP; 208 A; 171 C; 126 G; 220 T; 0 U; 0 Other;
      Improving immune response to HIV antigen by which comprises an antigen such as gp120 or chemokine, and carrier.
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                                                                                                                             Disclosure, Col 19-20; 40pp; English
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15-NOV-2001; 2001US-0334468P.
01-AUG-2002; 2002US-00210120.
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17-DEC-2001
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                 Raponi M;
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AAN91337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to a novel method of characterising prostate tissue in a subject and to compositions and methods for cancer diagnostics, including cancer markers, in particular prostate cancer. Prostate cancer (PCA) is a leading cause of male cancer-related death. Additional serum and tissue blomarkers would aid diagnosis. The invention may provide means of producing compounds with a cytostatic activity or allow the development of gene therapy. The methods of the invention useful for characterising prostate tissue in a subject, screening subject, detecting AMACR (alpha-methylacyl-coenzyme A racemace) expression in a bodily fluud, characterising the growth of cells. The diagnosing cancer in a subject and inhibiting the growth of cells. The present sequence is a DNA sequence which is preferably utilised in the
                     Characterizing prostate tissue comprises providing a prostate tissue sample from a subject and detecting the presence or absence of expression of hepsin, pim-1 or EZH2.
                                                                                                                                                                                                                                                                                                                                                                  123 CAGCCAGATGCAATGCCCCAGTCACTGCTTATAACTTCACCAATAGGAAGATC 182
                                                                                                                                                                                                                                                                                                                                                                                                         TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCCAAAGAAGCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT 302
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                                                                                                                                                                                                                                                                                                                                            1 CAGCCAGATGCAATGAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Farnesyl transferase inhibitor modulated leukemia associated gene #58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88; cytostatic; farnesyl transferase inhibitor; gene expression;
quinolinone; leukemia; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGGATICCATGGACCACCIGGACAGCAAACCCAAACTCCGAAGACT 350
                                                                                                                                                                                                                                                                                                  Length 725;
                                                                                                                                                                                                                                                                      Sequence 725 BP; 208 A; 171 C; 126 G; 220 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                               100.0%; Score 228; DB 9;
100.0%; Pred. No. 5.4e-62;
iive 0; Mismatches 0;
                                                                    Disclosure; SEQ ID NO 66; 297pp; English.
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2001US-0340938P.
2001US-0341012P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 228; Conservative
                                                                                                                                                                                                                                                  method of the invention.
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30-OCT-2001;
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The invention relates to a method of determining whether a patient will respond to treatment with a farnesyl transferase inhibitor (FTI), by analyzing the expression of gene that is differentially modulated in the presence of an FTI. The method is useful for determining whether a patient will respond to treatment with a FTI such as (B) 6-[amino(4-chlorophenyl) (1-methyl-1H-imidazol-5-yl)methyl] 4-(3-chlorophenyl) 1-methyl-2-(IA)quinolinone, monitoring the therapy of a patient, treating a patient with leukemia with FTI if the analysis indicates that the patient will respond. This sequence corresponds to a gene whose expression may be modulated in the presence of FTI.
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                                                             Determining whether a patient will respond to treatment with a farnesyl transferase inhibitor, by analyzing the expression of gene that is differentially modulated in the presence of the inhibitor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GIGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCCAAGCAGAAGTGGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 725 BP; 208 A; 171 C; 126 G; 220 T; 0 U; 0 Other;
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100.0%; Score 228; DB 9; I
Best Local Similarity 100.0%; Pred. No. 5.4e-62;
Matches 228; Conservative 0; Mismatches 0;
                                                                                                                                                                                                    Disclosure; SEQ ID NO 58; 346pp; English
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/*tag= c
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705. 709

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53. .350
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(revised)
(first entry)
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WPI; 2003-513497/48.
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The present sequence encodes a monocyte chemoattractant peptide (MCP) designated MCP-1. MCPs can be isolated from human glioma cell line U-105MG and peripheral blood mononuclear leukocytes. MCPs are used for the treatment of neoplasms and infections in humans. Short peptides derived from MCPs can be screened to identify those that can bind to the monocyte receptor without stimulating a chemotactic response. These are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 ergarctrcaagaccarreregeccaaggacterererereaccecaagcagaagregeri 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide with chemotactic activity for monocytes - from human monocytes or glioma cells, useful for treating infections and neoplasms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy; antiinflammatory; vulnerary; gynecological; ophthalmological; vaccine; hypoxia; tumourigenesis; angiogenesis; apoptosis; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GIGAICITCAAGACCAITGIGGCCAAGGAGAICIGIGCIGACCCCAAGCAGAAGIGGGIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CAGCCAGATGCAATCAATGCCCCAGCCTGCTGTTATAACTTCACCAATAGGAAGATC
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               /*tag= a /rtansl except= (pos: 54. .56, aa: Met) /transl except= (pos: 114. .116, aa: Gly) 707. .711 /*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.4e-62;
                                                                                                                                                                                                                                                                                                                                                                                  Robinson EA, Yoshimura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypoxia-regulated protein coding sequence #91.
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89US-00330446
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Best Local Similarity
Matches 228; Conserv
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                                                                                                                                                                                                                                                                         31-JAN-1989;
30-MAR-1989;
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                                                                                                                                                                                                                                06-JUN-1995;
                                                                                 polyA_signal
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                                                                                                                                               US5714578-A
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                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence encodes a human-derived monoyte chemo-attractant peptide product (MCP-1) which exhibits optimal chemotactic activity at a conco. of 1nM and has a mol. mass of ca. 8,400 D. MCP-1 can be used for treating infection eg inflammatory disease, or for the control of neoplasms by accumulation of monocytes at the site of the infection. The DNA is obtd. by chemical synthesis, by screening reverse trascribts of mRNA from purified blood leukocytes or cell cultures of eg U-373 MG or KMG-5. (Note: Revised entry submitted to correct the patent number format of US Government-owned NTIS applications to prevent clashes with orgaing US granted patent numbers. For further information please visit the Derwent web site at www.derwent.com/dwpl/updates/ntis_us.html.) (Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                                                                                         obtd. from human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monocyte chemoattractant peptide; MCP; MCP-1; treatment; neoplasm; infection; human; monocyte receptor; chemotactic response; inflammation; monocyte infiltration; ss.
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                                                                                                                                                                                                                                                                                                                    Human derived monocyte chemo:attractant peptide prods. - obtd. from h
glioma cell line U-105MG or peripheral blood mono:nuclear leukocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA encoding a macrophage chemoattractant peptide designated MCP-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 228; DB 1; Length 738; 100.0%; Pred. No. 5.4e-62; ive 0; Mismatches 0; Indels
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                                                                                                                        DEPT HEALTH & HUMAN SERVICE.
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SEC OF COMMERCE.
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                                             89US-00330446
                                                                                      89US-00304234
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                                             30-MAR-1989;
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    25-JUL-1989
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Query Match

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Indels

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Claim 37; Page 399; 538pp; English.
                                                                        (OXFO-) OXFORD BIOMEDICA UK LTD
                                                           08-FEB-2001; 2001GB-00003156.
25-OCT-2001; 2001GB-00025666.
                                              10-DEC-2001; 2001WO-GB005458
                                                                                                                                                                                                                                    100.08;
                                                                                                                                                                                                                                       Best Local Similarity 100.0%;
Matches 228; Conservative 0
                                                                                  Mundy CR,
                                                                                               WPI; 2002-627238/67.
                                                                                                                      regulated gene.
                           WO200246465-A2
                                                      08-DEC-2000;
                   Homo sapiens
                                                                                     Rayner WN;
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                                                                                  White J,
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ABZ34738 standard; cDNA; 739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to methods for identifying genes and proteins that are implicated in a specific disease or physiological condition. The method comprises comparing the transcriptome/proteome of a specialised cell type implicated in a disease or condition with that of a second specialised cell type, under two experimental conditions, and identifying a gene that is differentially regulated in the two specialised cell types under experimental conditions. ABN77873-ABN78116 and ABP65061-ABP65257 were identified using the methods of the invention. The coding sequences and proteins are useful for treating a disease in a patient, for manufacture of a medicament for treating hypoxia-regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conditions, and for regulating tumourigenesis, angiggenesis, apoptosis, biological response to hypoxia conditions, or hypoxic-associated abthology in a patient. The coding sequences and proteins are also useful for monitoring the therapeutic treatment of a disease or physiological condition, such as cancer, ischemic conditions, reperfusion injury, retinopathy, neonatal stress, preeclapmsia, atherosclerosis, inflammatory conditions, wound healing, inflammation, erythropoiesis or hair loss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAAGAAGATC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120
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ischaemic condition; reperfusion injury; retinopathy; neonatal stress; preeclapmsia; atherosclerosis; inflammatory condition; wound healing; inflammation; erythropoiesis; hair loss; human; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    two cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying a gene involved in disease for treating hypoxia-regulated conditions, comprises comparing the transcriptome/proteome of two celltypes under different conditions and identifying a differentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CAGCCAGATGCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 GTGATCTTCAAGACCATGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    Harris RA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT
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                                                                                                                                                                                                                                                                                                                                                                                                 Ward NR, Krige D, Kingsman SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 228; DB 6;
; Pred. No. 5.4e-62;
0; Mismatches 0;
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differentially expressed in models of osteogenesis upon being put in contact with a stimulator of osteogenesis. The present sequence is one such sequence. This sequence can be used for diagnosing osteoporosis/bone disease in a patient, promoting osteogenesis and/or preventing osteoporosis/bone disease. The present sequence encodes a secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grearcricaagaccarreregeccaagaarcrerereacceaagcagaagregerr 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention relates to novel nucleotide sequences, which are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           isolated nucleic acid upregulated/downregulated in osteogenesis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTTATAACTTCACCAATAGGAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CAGCCAGATGCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                  Osteopathic; osteogenesis modulator; gene therapy; osteogenesis; osteoporosis; bone disease; downregulator; human; ss.
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G;
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                                                Coding sequence SEQ ID 96, downregulated in osteogenesis.
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100.0%; Pred. No. 5.4e-62;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Call K, '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for bone disease therapy in subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 27; Page 124-125; 237pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bushnell SE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВЪ
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Matches 228; Conservative
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04-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Connolly T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Garcia T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Human adenosine receptor related polynucleotide SEQ ID NO:2588.

RESULT 14 ABZ34738

Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothioate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; attifinflammatory; antiallergic, antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss. Homo sapiens.

WO200009525-A2

24-FEB-2000.

99WO-US017712. 03-AUG-1999; 98US-0095212P. 03-AUG-1998;

(UYEC-) UNIV EAST CAROLINA

Nyce JW;

WPI; 2000-205971/18.

New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstruction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or

Disclosure; Page 761-762; 1343pp; English.

The present invention describes a new composition comprising an antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets coligonucleotide acids involved in bronchoconstraction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating c. impaired airways, including lung diseases associated with inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, emphysema, chronic obstructive fibrosis, and cancers which may metastasis to the lungs, including breast and prostate cancer. The reduction of the adenosine content of the owns reduces side effects. The A-containing ONS break down with the release of deoxyadenosine which activates adenosine receptors causing bronchoconstriction and inflammation. AAA12313 to AAA3531 represent to invention, which correspond to SEQ ID No:1 to 188, but the sequences differ from the previously named sequences. SEQ ID No:1 to 188, but the sequence of from the previously named sequences. SEQ ID No:1 to 188, but the sequence of from the previously named sequences. SEQ ID No:1 to 188, but the sequence of from the present invention. N. B. Sequences given in the disclosure of the present invention. N. B. Sequences given in the sequence given in the sequence given in the sequence given in the sequence of the present invention. isting

Sequence 741 BP; 214 A; 173 C; 133 G; 221 T; 0 U; 0 Other;

ö Gaps ö 100.0%; Score 228; DB 3; Length 741; 100.0%; Pred. No. 5.5e-62; ive 0; Mismatches 0; Indels C Query Match 100. Best Local Similarity 100. Matches 228; Conservative

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258 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCCAAAGAAGCT 199 reagrecadadecredecadecraradadaareaceadeadeaagaagera 61

121 GIGAICTICAAGACCATIGIGGCCAAGGAGAICTGIGCIGACCCCAAGCAGAAGIGGGIT 180 259 grgarcricaagaccarreregeccaagaarcrererecceaeccaagcaaagaagreerr CAGGATTCCATGGACCACCTGGACAAGCAAACCCCAAACTCCGAAGACT 228 319 caggatrocardgaccaccrogacaagcaaacccaaacrocgaagacr 366 181 q ò g à

completed: August 31, 2004, 02:58:29 ne : 241 secs Search cor Job time

Luis Page Blank (uspio)

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM nucleic - nucleic search, using sw model

Run on:

August 30, 2004, 16:49:11; Search time 54 Seconds (without alignments) 2343.126 Million cell updates/sec

07330446 228 1 cagccagatgcaatcaatgc.....aaaacccaaactccgaagact 228 Title: Perfect score: Sequence:

682709 seqs, 277475446 residues IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Searched:

Scoring table:

1365418 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	equence 3,	equence 134	equence 25,	equence 116	equence 106	equence 105	Sequence 2, Appli	m		50	equence 30,	13	equence 127	15,	equence 17,	901	equence 26,	equence 978	10	equence 115	equence 28,	'n	'n	'n	ω̈	Seguence 25, Appl	1234, A
	ID	1-992-	-09-023-655-1	-07-927-39	-09-023-655-11	-09-148-545-1	-148-545-10	T-US95-00605-	08-250-958-	2	3-451	-09-463-451-3	-927-391-1	-09-016-434-1	-07-92	-07-927-391-1	-09-023-655-90	-09-366-8	-09-023-655-97	-09-016-434-10	-09-016-434-115	-09-463-458A-2	1	-09-545-89	-744-419-	09-463-45	US-09-463-458A-25	US-09-833-381-1234
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	Length	725	725	741	741	1712	1822	231	228	752	213	213	228	810	814	247	294	605	807	840	813	207	315	514	540	207	207	400
	Match	100.0	100.0		00			99.3	•													•					58.9	
	Score	228	228	228	228	27	27	226.4	24	17	196	196	48	48	æ	47	39	σ	139.6	139	138	135.4	135	135	135	34	134.4	7
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RESULT 2 US-09-023-655-1344 ; Sequence 1344, Application US/09023655

Sequence 3, Appli Sequence 1, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 31, Appli Sequence 32, Appli Sequence 33, Appli Sequence 34, Appli Sequence 45, Appli Sequence 45, Appli Sequence 45, Appli	845 122 21,
US-08-613-822-3 US-08-852-12-1 US-09-261-201A-3 US-09-261-201A-3 US-09-177-209-3 US-09-16-887A-15 US-09-545-894-1 US-09-546-028-39 US-09-646-028-39 US-09-646-028-37 US-09-646-028-37 US-09-646-028-37 US-09-646-028-37 US-09-646-028-37 US-09-646-028-37 US-09-646-028-37 US-09-646-028-37	US-09-023-655-845 US-09-833-381-1229 US-09-366-887A-21
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ALIGNMENTS

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Page

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APPLICANT: MILOUX, Brigitte
APPLICANT: MILOUX, Adrian
APPLICANT: MILOUX, Adrian
APPLICANT: MIRY, Adrian
APPLICANT: WIRY, Adrian
TITLE OF INVENTION: activity, and recombinant DNA, expression vector and hosts
TITLE OF INVENTION: for its preparation.
TITLE OF INVENTION: for its preparation.
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: King Street Station, Suite 500,1800 Diagonal
STREET: Road, PO Box 299
CITY: ALEXANDRIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                139 cagccagargcaarcaargccccagrcacrcrcrcrraraacrrcaccaaragaagarc 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259 GIGAICTICAAGACCAITGIGGCCAAGGAGAICTGIGGGTGACCCCAAGCAGAAGIGGGTT
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Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
APPLICANT: Coffrey J. Sailhamer
TITLE OF INVENTION: EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CAGCCAGATGCAATGCCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 228; DB 3; Length 741;
Best Local Similarity 100.0%; Pred. No. 3.8e-61;
Matches 228; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                    WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/927,391
FILING DATE: 1992029
CLASSIFICATION: 530
ATTONNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard
D REGISTRATION NUMBER: 28,665
REPERENCE/POCKET NUMBER: 16781/369
TELEPROMYNICATION INFORMATION:
TELEPROMYNICATION INFORMATION:
TELEPROMYNICATION: (703) 836-9300
TELEPRA: (703) 683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELBEAK: (''U.,
TELEFAK: (''U.,
TELEEX: 899149
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 741 base pairs
""OR: NUCLEIC ACID
""OR: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                            ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
FERRARA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                               VIRGINIA
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US-09-023-655-1165
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                                             APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILLING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 228; DB 4;
100.0%; Pred. No. 3.8e-61;
ive 0; Mismatches 0;
                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY FACENT INFORMATION:
ATTORNEY FAGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECHONE: (650) 855-0555
TELECHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1344:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                 ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMEDTURTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
US-07-927-391-25
; Sequence 25, Application US/07927391
; Patent No. 6001649
; GENERAL INFORMATION:
APPLICANT: CAPUT, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 725 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                            CITY: PALO ALTO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                             GENERAL INFORMATION:
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US-09-023-655-1344
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                                                                                                                                                                                                                                                                                                                                 USA
  Patent No. 6607879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Simi
Matches 228;
                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY:
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139 CAGCCAGATGCAATGCCCCCAGTCACTGCTTATAACTTCACCAATAGGAAGATC 198
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                                                                                                                                              COUNTRY: USA

ZIP: 94304

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
APPLICATION UNDBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION NUMBER: 37,037
PRIOR APPLICATION DATA:
PRIOR APPLICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
TLASSIFICATION:
TALESTRICATION NUMBER: 37,031
REFERENCE/DOCKET NUMBER: 37,031
REFERENCE/DOCKET NUMBER: 37,031
REFERENCE/DOCKET NUMBER: 660) 845-4166
INFORMATION FOR SEQ ID NO: 1165:
SEQUENCE CHARACTERISTICS:
LENGTH: 741 base pairs
TYPE: nucleic acid
STATE: nucleic acid
STATE: INCOLOGY: linear
INMEDIATE SOURCE:
LENGTH: 9187434
US-09-023-655-1165
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE PADRESS:
STREET: 3174 PORTER DRIVE
STREET: PALO ALTO
STREET: CITY: PALO ALTO
STRATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 228; Conserva'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
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RESULT 5
US-09-148-545-106
Sequence 106, Application US/09148545
Sequence 106, Application US/09148545
Sequence 106, Application US/09148545
SEQUENCE NO. 6590075
TITLE OF INVENTION: 70 Human Secreted Proteins
FIRE REFERENCE: PS001PL
CURRENT APPLICATION NUMBER: US/09/148,545
CURRENT FILING DATE: 1998-09-04
EARLIER FILING DATE: 1998-03-06
EARLIER PULICATION NUMBER: 60/040,162

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R APPLICATION NUMBER: 60/056,864
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,631
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,845
R FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R FILING DATE: 1997-05-23
R PELLING DATE: 1997-05-23
R FILING DATE: 05-8ep-1997
R APPLICATION NUMBER: 60/047,599
R APPLICATION NUMBER: 60/047,588
R APPLICATION NUMBER: 60/047,588
R PILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,313
PILING DATE: 1997-04-11
PELING DATE: 1997-04-11
PILING DATE: 1997-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,872
FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/056,882
FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1997-08-22
APPLICATION WUMBER: 60/056,892
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/047,595
                                                                                                                                                                                                                                                       FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,889
                                                                                                                                                                                                                                                                                                                                                                                                                                          LING DATE: 1997-08-22
PLICATION NUMBER: 60/056,662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/056,888
FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/056,911
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,636
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,910
FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,590
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,594
                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/056,877
                                                                                                                                                                                                                                                                                                                            PLICATION NUMBER: 60/056,893
                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/056,630
                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,878
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PPLICATION NUMBER: 60/056,903
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FILING DATE: 1997-08-22
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1179 ergarcricaagaccarreregecaaggagarcrerecreacceaagcagagagregerr 1238 1059 CAGCCAGATGCAATGCCCCAGTCACCTGCTGYTATAACTTCACCAATAGGAAGATC 1119 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGGAGTGTCCCAAAGAAGCT 61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT 1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC 121 GIGAICTICAAGACCAITGIGGCCAAGGAGAICTGIGCTGACCCCAAGCAGAAGTGGGIT Gaps ; 0 Length 1712; 181 CAGGATTCCATGGACCACCTGGACAAGCAAACCCCAAACTCCGAAGACT 228 Query Match 99.8%; Score 227.6; DB 4; Length Best Local Similarity 99.6%; Pred. No. 6.9e-61; Matches 227; Conservative 1; Mismatches 0; Indels EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-06-22
EARLIER FILING DATE: 1997-06-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-0 AFFLING DATE: 1997-05-22
APPLICATION NUMBER: 60/047,593 RESULT 6 US-09-148-545-105 LENGTH: 1712 ଟ ઠ

1178

Sequence 105, Application US/09148545
Patent No. 6590075
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: PZ001P1

CURRENT FILING DATE: 1998-09-04

EARLIER APPLICATION NUMBER: 108/09/148,545

EARLIER PLILION DATE: 1998-09-04

EARLIER PLILION DATE: 1998-03-06

EARLIER PLILION DATE: 1997-03-07

EARLIER PLILION DATE: 1997-05-03

EARLIER PLILION DATE: 1997-05-0

BARLIER FILING DATE: 1997-04-11
BARLIER APPLICATION NUMBER: 60/043,674
BARLIER APPLICATION NUMBER: 60/043,669
BARLIER APPLICATION NUMBER: 60/043,669
BARLIER FILING DATE: 1997-04-11
BARLIER APPLICATION NUMBER: 60/043,315
BARLIER FILING DATE: 1997-04-11
BARLIER FILING DATE: 1997-06-06
BARLIER FILING DATE: 1997-06-06
BARLIER FILING DATE: 1997-06-02
BARLIER FILING DATE: 1997-06-02
BARLIER FILING DATE: 1997-06-02
BARLIER FILING DATE: 1997-06-22
BARLIER PILING DATE: 1997-06-22
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61 TCAGTGCAGAGGTTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 228
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GENERAL INFORMATION:

APPLICANT: Lyle, Leon
APPLICANT: Thoms-Alller, Beth
TITLE OF INVENTION: THERAPEUTIC TREATMENT FOR INHIBITING
TITLE OF INVENTION: VASCULAR RESTENOSIS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mallinckrodt Medical, Inc.
STREET: 675 McDonneil Boulevard, P.O. Box 5840
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 63134
COMPUTER READBLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TIM PC compatible
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PS-LECHIIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 13-JAN-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Monocyte Chemotactic Protein-1 STRAIN: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/182,917
FILING DATE: 14-JAN-1994
APPLICATION NUMBER: US 07/965,678
FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Vacca, Rita D.
REGISTRATION NUMBER: 33,624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33,624
3R: 0783.2
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TELECOMMUNICATION:
TELEPHONE: 314-895-7215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 314-895-2156
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 base pairs
TYPE: nucleic acid
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STATE: Missouri
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TOPOLOGY: lir
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PCT-US95-00605-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1349 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 1396
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                                                          EARLIER FILLING DATE: 1997-09-28
EARLIER FILLING DATE: 1997-05-23
EARLIER FILLING DATE: 1997-05-23
EARLIER FILLING DATE: 1997-05-23
EARLIER FILLING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,589
EARLIER APPLICATION NUMBER: 60/047,589
EARLIER APPLICATION NUMBER: 60/047,593
EARLIER FILLING DATE: 1997-05-23
EARLIER FILLING DATE: 1997-05-23
EARLIER FILLING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,578
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILLING DATE: 1997-04-11
EARLIER FILLING DATE: 1997-04-11
EARLIER FILLING DATE: 1997-04-11
EARLIER FILLING DATE: 1997-04-12
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER APPLICATION NUMBER: 60/056,654
EARLIER APPLICATION NUMBER: 60/056,654
EARLIER APPLICATION NUMBER: 60/056,654
EARLIER FILLING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,654
EARLIER FILLING DATE: 1997-08-22
EARLIER RAPLICATION NUMBER: 60/056,654
EARLIER RAPLICATION NUMBER: 60/056,664
EARLIER RAPLICATION NUMBER: 60/056,691
EARLIER RAPLICATION NUMBER: 60/056,664
EARLIER RAPLICATION NUMBER: 60/056,664
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EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-25
EARLIER FILING DATE: 1997-08-25
EARLIER FILING DATE: 1997-08-25
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EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-25
EARLIER FILING DATE: 1997-08-26
EARLIER APPLICATION NUMBER: 60/056, 908
EARLIER APPLICATION NUMBER: 60/056, 904
EARLIER PILING DATE: 1997-08-06
EARLIER FILING DATE: 1997-08-05
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-08-05
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EARLIER FILING DATE: 1997-08-05
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                                     LING DATE: 1997-05-23
PLICATION NUMBER: 60/047,590
LING DATE: 1997-05-23
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Best Local Similarity
Matches 227; Conserv.
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RESULT 8 US-08-250-958-3 ; Sequence 3, Application US/08250958 ; Patent No. 5571713

Gaps

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DB 6;
                                                                                                                                                                             Query Match
95.4%; Score 217.4; DB 6;
Best Local Similarity 99.5%; Pred. No. 7.2e-58;
Matches 218; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Fillsbury Madison & Sutro, STREET: 1100 New York Avenue, N.W. CITY: Washington STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORG
CURRENT APPLICATION NUMBER: US/09/463,451
FILING DATE: 03-Apr-2000
CLASSIFICATION NUMBER: US/09/463,451
FILING DATE: 21-AUL-1998
FILING DATE: 21-JUL-1998
FILING DATE: 21-JUL-1998
RILING DATE: 25-JUL-1997
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS: 23-JUL-1997
INFORMATION FOR SEQ ID NO: 29:
LEWITH APPLICATION NUMBER: 25-JUL-1997
INFORMATION FOR SEQ ID NO: 29:
LEWITH APPLICATION NOT APPLICATION FOR SEQ ID NO: 29:
LEWITH APPLICATION NOT APPLICATION FOR SEQ ID NO: 29:
LEWITH APPLICATION NOT APPLICATION FOR SEQ ID NO: 29:
LEWITH APPLICATION NOT APPLICATION FOR SEQ ID NO: 29:
LEWITH APPLICATION 
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLGGY: linear
MOLECULE TYPE: other nucleic acid
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 29, Application US/09463451; Patent No. 6537779
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KARA, Buhpendra V. PIOLI, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 97.55
Matches 199; Conservative
FILING DATE:12-MAY-1989; SEQ ID NO:1:
                                                                               LENGTH: 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
US-09-463-451-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-463-451-29
                                                                                                                5212073-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 UCAGUGCAGAGGCUCGCGAGCUADAGAAUCACCAGCAGCAAGUGUCCCAAAGAAGAU 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CAGCCAGAUCAAUCACCCCAGUCACCUGCUGUUAUAACUUCACCAAUAGGAAGAUC 60
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5212073-1
; Patent No. 5212073
; APPLICANT: ROLLINS, BARRETT; STILES, CHARLES; WONG, GORDON G.
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMAN JE CYTOKINE
NUMBER OF SEQUENCES: 1
CURRENT APPLICATION DATA:
CHARRENT APPLICATION DATA:
JAPPLICATION NUMBER: US/07/351,008
          GENERAL INFORMATION:
APPLICANT: LYLE, LEON R.
APPLICANT: WINKEL, STEVEN L.
APPLICANT: STRIETER, ROBERT M.
TITLE OF INVENTION: THERAPECUTIC TREATMENT FOR INHIBITING
TITLE OF INVENTION: VASCULAR RESTENOSIS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rethwell, Figg, Ernst & Kurz
STREET: Suite 701-E, 555 Thirteenth St., N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.

ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYDE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250,958
FILING DATE: 27-MAY-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: 07/965,678
FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: WALKER, Barbara W.
REGISTRATION NUMBER: 35,400
REFREENCE/DOCKET NUMBER: 30,770-206A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION ON: 3:
SEQUENCE CHARACTERESTICS:
LENGTH: 228 base pairs
TYPE: nucleic acid
STANDEDINESS: single
TYPE: nucleic acid
STANDEDINESS: single
TYPE: NOLECULE TYPE: MRNA
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80.7%; Pred. No. 2.4e-60;
tive 42; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                       CITY: Washington STATE: D. C. COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 184; Conserv
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US-08-250-958-3
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61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT 120
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                                                                                                                                                                                                                                                                                                                                                                         162 GTGATCTTCAAGACCATTGTGGCCAAGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT 321
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                                                                                                           1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
                                                     Gaps
                                                  ;
0
Length 752;
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HOCKNEY, Robert C.
TITLE OF INVENTION: T' Promoter-Based Expression System
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.0%; Score 196; DB 4; Length 213; 97.5%; Pred. No. 1.9e-51; Live 0; Mismatches 5; Indels
                                                  Indels
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Sequence 13, Application US/07927391

Batent No. 6001649

GENERAL INFORMATION:
APPLICANT: CAPUT, Daniel
APPLICANT: FERRARA, Pascual
APPLICANT: MINCUX, Brigitte
APPLICANT: WITMY, Adrian
APPLICANT: WITMY, Adrian
APPLICANT: WITMY, Natalio
TITLE OF INVENTION: Protein having a cytokin type
TITLE OF INVENTION: protein having a cytokin type
TITLE OF INVENTION: for its preparation.
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GTAATCTTCAAGACCAAACTGGACAAGGAGATCTGTGCTGCTGACCCCACAGAAGTGGGTC 180
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STREET: Folsy & Larbner
STREET: King Street Station, Suite 500, 1800 Diagonal
STREET: Road, PO Box 299
STREET: VIRGINIA
STATE: VIRGINIA
STATE: VIRGINIA
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.0%; Score 148.2; DB 3; 78.7%; Pred. No. 1.1e-36; ive 0; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 19920929
CLASSIFICATION: 530
                           205 AAGCAAACCCAAACTCCGAAGACT
                                                    30 AAGCAAACCCAAACTCCGAAGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D
REGIGTRATION NUMBER: 28,665
REFERNCE/DOCKET NUMBER: 1678:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA (genomic)
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Matches 177; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 228 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                           RESULT 12
US-07-927-391-13
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                                                                                                                  64 AGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCTGTGATCTTCAAGACCATTGTGGCC 123
                                                                                                                                                                  145 AAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGATTCCATGGACCACCTGGAC 204
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84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 GTCACCTGCTGTTATAACTTCACCAATAGGAAGATCTCAGTGCAGAGGCTCGCGAGCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 AGAAGAATCACCAGCAGCAGTGTCCCAAAGAAGCTGTGATCTTCAAGACCATTGTGGCC
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Patent No. 6537779
GENERAL INFORMATION:
APPLICANT: KARA, Buhpendra V.
PIOLI, David
BUNDELL, Kenneth R.
HOCKNEY, DOCKNEY, TO PROMET C.
TITLE OF INVENTION: T7 Prometer-Based Expression System NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86.0%; Score 196; DB 4; Length 213; 97.5%; Pred. No. 1.9e-51; ive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/463,451
FILLING DATE: 03-APPL-2000
CLASSIFICATION: cURKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/GB98/02175
FILING DATE: 21-JUL-1998
APPLICATION NUMBER: GB 9715660.8
FILING DATE: 25-JUL-1997
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
                                                                                                                                                                                                                                                            205 AAGCAAACCCAAACTCCGAAGACT 228
                                                                                                                                                                                                                                                                                                      AAGCAAACCCAAACTCCGAAGACT 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 213 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 97.5
Matches 199; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       US-09-463-451-30/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-463-451-30
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181 CAGGACTITATGAAGCACCTGGACAAGAAAACCCAAACTCCAAAG 225

Page

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Sequence 15, Application US/07927391
Patent No. 6001649
GENERAL INFORMATION:
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NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY:
; LOCATION:
US-07-927-391-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        임
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 cadccadridagarraharrahacraccidcideracaarraharahadaahrah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 GTGATCTTCAAGACCATTGTGGCCCAAGGAGATCTGTGCTGACCCCCAAGCAGAAGTGGGTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                260 GTAATCTTCAAGACCAAACTGGACAAGGAGATCTGTGCTGACCCCACACAGAAGTGGGTC 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC 60
                                                                                      Sequence 1273, Application US/09016434

Sequence 1273, Application US/09016434

Patent No. 6500938

GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
ITILE OF INVENTION: PATHWAY GENE EXPRESSION
ITILE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SECUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSES: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STREET: ALTORINA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATION:
COMPUTER: IBM PC COMPATION:
COMPUTER: IBM PC COMPATION:
COMPUTER: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
CHING DATE: HEREWITH
FILING DATE: HEREWITH
FILING DATE: HEREWITH
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAG 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER:
FILLIG DATA:
CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 97,071
RELEPHONE: (650) 845-4166
INFORMATION FOR SEG ID NO: 1273:
ERNGTH: 810 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
IMMEDIATE SOURCE:
IMMEDIATE SOURCE:
IMMEDIATE SOURCE:
ILBRARK: GENBANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLONE: 9288396
US-09-016-434-1273
                                                                                 US-09-016-434-1273
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RESULT 14

General involvation:
APPLICANT: CAPUT, Daniel
APPLICANT: FERRARA, Pascual
APPLICANT: FERRARA, Pascual
APPLICANT: MIGUX, Brigite
APPLICANT: MIGUX, Brigite
APPLICANT: MINTY, Adrian
APPLICANT: VITA, Nataio
TITLE OF INVENTION: Protein having a cytokin type
TITLE OF INVENTION: for its preparation.
TITLE OF INVENTION: for its preparation.
MUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: King Street Station, Suite 500,1800 Diagonal
STREET: Road, PO Box 299
CITY: ALEXANDRIA
STATE: VIRGINIA
COUNTRY: USA 140 CAGCCAGTTGGGATTAATACTTCAACTACCTGCTGCTACAGATTTATCAATAAGAAAATC 199 121 GTGATCTTCAAGACCATTGTGGCCCAAGGAGATCTGTGCTGACCCCCAAGCAGAAGTGGGTT 180 260 GTAATCTTCAAGACCAAACTGGACAAGGAGATCTGTGCTGACCCCACACAGAAGTGGGTC 319 1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC ., Length 814; Indels COUNTRY: UGA

ZIP: 2231-0299
COUNTRY: UGA

ZIP: 2231-0299
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-Base #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/927,391
FILING DATE: 1992029
CLASSIFICATION: 530
ATTONEY/AGENT INFORMATION:
NAME: SAXE Bernhard
NAME: SAXE Bernhard
NAME: 28.665
REGISTRATION NUMBER: 28,665
REFERENCE/POCKET WUMBER: 16781/369
TELEFAX: (703) 836-9300
TELEFAX: (703) 836-9300
TELEFAX: (703) 833-4109
TELEFAX: (703) 833-4109
TELEFAX: (703) 683-4109
TELEFAX: (703) 683-4109
TELEFAX: (703) 683-4109
TELEFAX: (703) 683-4109
TELEFAX: (703) 683-6105
TELEFAX: (703) 683-6105 Query Match 65.0%; Score 148.2; DB 3; Best Local Similarity 78.7%; Pred. No. 1.8e-36; Matches 177; Conservative 0; Mismatches 48;

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Sequence 17, Application US/07927391

Sequence 17, Application Description Descrip
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Best Local Similarity 78.6%; Pred. No. 2.4e-36;
Matches 176; Conservative 0; Mismatches 48; Indels 0.
181 CAGGATTCCATGGACCACCTGGACAAGCAAACTCCGAAG 225
                                                    320 CAGGACTITAIGAAGCACCTGGACAAGAAAACCCAAACTCCAAAG 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGGACTITATGAAGCACCTGGACAAGAAAACCCCAAACTCCAAA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/927,391
FILING DATE: 19920929
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D
REGISTRATION NUMBER: 28,665
REFRENCE/DOCKET NUMBER: 16781/369
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS: LENGTH: 247 base pairs TYPE: NUCLEIC ACID STRANDEDNESS: double TOPOLOGY: linear COS-927-391-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (703) 683-4109
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Search completed: August 31, 2004, 02:59:28 Job time : 56 secs

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August 31, 2004, 02:59:34; Search time 254 Seconds (without alignments) 4417.658 Million cell updates/sec
                                                                                                                                                                                                   07330446
228
1 cagccagatgcaatcaatgc.....aaacccaaactccgaagact
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                3237270 seqs, 2460713050 residues
                                                                                - nucleic search, using sw model
                                                                                                                                                                                                                                                                                     IDENTITY NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                     Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                  OM nucleic
                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                         Run on:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Published Applications NA:*

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| cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
| cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
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| cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
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                                      Database :
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	laten	Length	3 :	10	Description
	0.001		15	US-10-276-971-3	Sequence 3, Appli
	100.0		13	US-10-449-831A-209	Seguence 209, App
	100.0		13	US-10-449-831A-213	Sequence 213, App
	100.0		15	US-10-060-036-3105	Seguence 3105, Ap
	100.0		σ	US-09-777-430A-72	Sequence 72, Appl
228	100.0	725	15	US-10-210-120-66	Sequence 66, Appl
	100.0		17	US-10-641-643-1344	Sequence 1344, Ap
	100.0		17	US-10-283-975A-58	Seguence 58, Appl
	100.0		17	US-10-764-649-17	Seguence 17, Appl
	100.0		13	US-10-342-887-849	Sequence 849, App
	100.0		13	US-10-172-118-849	Sequence 849, App
228	100.0		13	US-10-170-385-396	Seguence 396, App
	100.0		17	US-10-641-643-1165	Seguence 1165, Ap
	100.0		15	US-10-133-013-210	Sequence 210, App

Sequence 377, App Sequence 19, Appli Sequence 189, Appl Sequence 52, Appl Sequence 52, Appl Sequence 52, Appl Sequence 54, Appl Sequence 54, Appl Sequence 106, App Sequence 106, App Sequence 106, App Sequence 105, Appl Sequence 1073, Appl Sequence 1173, Appl Sequence 1174, Appl Sequence 1174, Appl Sequence 1174, Appl Sequence 11774, Appl Sequence 11774	
US-10-388-360-377 US-10-339-778-1 US-10-339-778-1 US-10-34-090-583 US-09-971-4298-18 US-09-792-793A-52 US-09-792-793A-53 US-09-792-793A-53 US-09-792-793A-54 US-09-792-793A-54 US-09-792-793A-54 US-09-792-793A-54 US-09-792-793A-54 US-09-981-876-106 US-09-981-876-106 US-09-981-876-106 US-09-981-876-106 US-09-981-876-106 US-09-981-876-106 US-09-981-876-106 US-09-981-876-106 US-09-981-876-105 US-10-133-013-11 US-10-133-013-11 US-10-144-090-837 US-10-144-090-837 US-10-717-597-95	
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                     61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT 120
                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                            1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
                                                                                                                                                                                                                                              1 CAGCCAGATGCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                           0;
                                                                                                                                                                                                      Length 228;
                                                                                                                                                                                                     Query Match 100.0%; Score 228; DB 15; Length 22. Best Local Similarity 100.0%; Pred. No. 6.4e-66; Matches 228; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Human
US-10-276-971-3
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Length 405;

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RESULT 5
US-09-777-430A-72
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                                                                                                                                  Sequence 209, Application US/10449831A
Publication No. US20040029179A1
SEQUENCE 209, Application US/10449831A
Publication No. US20040029179A1
APPLICANT: Koentgen, Frank
TITLE OF INVENTION: Higher molecular weight entities and uses therefor Fils REPERENCE: 2385978
CURRENT FILING DATE: 2003-05-30
PRIOR APPLICATION NUMBER: USSN 60/384878
PRIOR PILING DATE: 2002-05-31
PRIOR FILING DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 237
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
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Publication No. US20040029179A1
GENERAL INFORMATION:
APPLICANT: Koentgen:
Frank
TITLE OF INVENTION: Higher molecular weight entities and uses therefor
FILE REPRENCE: 2385978
CURRENT APPLICATION NUMBER: US/10/449,831A
CURRENT APPLICATION NUMBER: USSN 60/384878
PRIOR PILING DATE: 2003-05-30
PRIOR PILING DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 237
SOFTWARE: Patentin version 3.2
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181 CAGGATTCCATGGACCACCTGGACAAGCAAACCCCAAACTCCGAAGACT 228
                      181 CAGGATTCCATGGACCACAGGACAAACCCCAAACTCCGAAGAT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 228; DB 13; Length 294; Best Local Similarity 100.0%; Pred. No. 7.1e-66; Matches 228; Conservative 0; Mismatches 0; Indels 0.
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OTHER INFORMATION: Human MCP-1 chimeric construct
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(294)
US-10-449-831A-209
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; LOCATION: (1)..(399)
US-10-449-831A-213
                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Human
                                                                                                                         US-10-449-831A-209
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US-10-449-831A-213
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LENGTH: 294
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LENGTH: 405
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145 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTTATAACTTCACCAATAGGAAGATC 204
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| Sequence 3105, Application US/10060036
| Sequence 3105, Application US/10060036
| Publication No. US20030073144A1
| GENERAL INFORMATION:
| APPLICANT: Benson, Darin R. APPLICANT: Lodes, Michael D. APPLICANT: Lodes, Michael J. APPLICANT: Hepher, William T. APPLICANT: Jiang, Yudiu
| APPLICANT: Jiang, Yudiu
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER PILE REFERENCE: 220121.566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  325 CAGGATTCCATGGACCACCTGGACAAGCAAACCCCAAACTCCGAAGAT 372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 CAGGATTCCATGGACCACCTGGACAAGCAAACCCCAAACTCCGAAGACT
                                                                            Indels
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100.0%; Score 228; DB 13;
100.0%; Pred. No. 8e-66;
Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/060,036
CURRENT FILING DATE: 2002-01-30
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                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-10-060-036-3105
                                             Similarity
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US-10-641-643-1344
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APPLICANT: Skrzypczynski, Zbigniew
APPLICANT: Allawi, Hatim T.
APPLICANT: Wayland, Sarah R.
APPLICANT: Wayland, Sarah R.
APPLICANT: Takowa, Tsetska
APPLICANT: Neir, Bruce P.
TITLE OF INVENTION: Charge Tags and the Separation of Nucleic Acid Molecules
FILE PEPERSANCE: FORS-04912
CURRENT APPLICATION NUMBER: US/09/777,430A
CURRENT FILING DATE: 2001-02-06
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin version 3.1
LENGTH: 647
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match
100.0%; Score 228; DB 9; Length 647;
Best Local Similarity 81.6%; Pred. No. 9.7e-66;
Matches 186; Conservative 42; Mismatches 0; Indels
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Sequence 66, Application US/10210120

Publication No. US20030175736A1

GENERAL INFORMATION:
APPLICANT: Chinnaiyan, Arul M.
APPLICANT: Chinnaiyan, Arul M.
APPLICANT: Rubin, Mark A.
TITLE OF INVENTION: Expression Profile of Prostate Cancer TILE REFERENCE: UM-07221

CURRENT FILING DATE: 2002-08-01

PRIOR PILING DATE: 2001-08-02

PRIOR PILING DATE: 2001-08-02

PRIOR PILING DATE: 2001-08-02

PRIOR FILING DATE: 2001-11-15

NUMBER OF SEQ ID NOS: 123

SOFTWARE: Patentin Version 3.2

SEQ ID NO 66

LENGTH: 725
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100.0%; Score 228; DB 15;
Best Local Similarity 100.0%; Pred. No. 1e-65;
Matches 228; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                      ; TYPE: RNA
; ORGANIGM: Artificial Sequence
; FEATURE:
; CTHER INFORMATION: Synthetic
US-09-777-430A-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
CRGANISM: Homo sapiens
US-10-210-120-66
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                                                                                                                                                                                                            243 GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCCAAGCAGAAGTGGCTT
183 TCAGTGCAAAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT
                                                                                                                                   121 GTGATCTTCAAGACCATTGTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT
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ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC competible
COMPUTER: IBM PC competible
COMPUTER: IBM PC Competible
COMPUTER: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
COMPUTER: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CLASSIFFCATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
CLASSIFFCATION NUMBER: ADARDACE
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 97,071
REFERENCE/DOCKET NUMBER: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1344, Application US/10641643
Sequence 1344, Application US/10641643
Publication No. US20040077003A1
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
Sugan G. Stuart
Jeffrey J. Seilhamer
Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD
GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 725;
                                                                                                                                                                                                                                                                                                                                                                                        303 caggatrccardgaccaccrdgacaagcaaacccaaagacr 350
                                                                                                                                                                                                                                                                                                           181 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 1e-65;
Matches 228; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC
STREET: 3174 FORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
SEQUENCE DESCRIPTION: SEQ ID NO: 1344
US-10-641-643-1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear IMMEDIATE SOURCE:
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121

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Best Local Similarity 100.
Matches 228; Conservative
                                                                                                                 ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (54)...(353)
US-10-764-649-17
                                                                     TYPE: DNA ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo
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; ORGANISM: Homc
US-10-342-887-849
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APPLICANT: Xu, Halyan
APPLICANT: Xu, Halyan
APPLICANT: Xu, Halyan
APPLICANT: Chen, Hong
APPLICANT: Chen, Hong
APPLICANT: Chen, Hong
APPLICANT: Chen, Hong
APPLICANT: Barnes, Olem
TITLE OF INVENTION: METADOLE DISORDERS
FILE OF INVENTION: METADOLE DISORDERS
FILE REFERENCE: MP12003-025PIRNM
CURRENT APPLICATION NUMBER: US/10/764,649
PRIOR APPLICATION NUMBER: 60/446041
PRIOR APPLICATION NUMBER: 60/446041
NUMBER OF SEQ ID NOS: 20
243 GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT 302
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                                                                                                                                                                                                                                           Sequence 56, Application US/10283975A
Sequence 56, Application US/10283975A
Publication No. US20040110792A1
Sequence 56, Application.
Sequence 56, Application.
TIPLE OF INVENTION:
TILE REFERENCE: COS 293 FOT
FILE REFERENCE: COS 293 FOT
FILE REPERENCE: COS 293 FOT
CURRENT APPLICATION NUMBER: US/10/283,975A
CURRENT FILING DATE: 2002-10-30
PRIOR FILING DATE: 2001-10-30
SOFTWARE: Patentin Version 3.1
SEQ ID NO 58
LENGTH: 725
                                                                                      181 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 228
                                                                                                                                   303 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 350
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100.0%; Score 228;
Best Local Similarity 100.0%; Pred. No. 1e
Matches 228; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: HUMAN
US-10-283-975A-58
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APPLICANT: Dai, Hongvue
APPLICANT: He, Yudong
APPLICANT: Linsley, Peter S.
APPLICANT: Linsley, Peter S.
APPLICANT: Moberts, Christopher J.
APPLICANT: Noberts, Christopher J.
APPLICANT: Van 't Veer' Laura Johanna
APPLICANT: Van 't Veer' Laura Johanna
APPLICANT: Van 't Veer' Laura Johanna
APPLICANT: Van 'd Veer' Laura Johanna
APPLICANT: Van 'd Veer' Laura Johanna
APPLICANT: Nor 't Veer' Laura Johanna
APPLICANT: Bernards, Rene
FILE REFERENCE: 301-188-99
CURRENT FILING DATE: 2003-01-18
PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
SPIOR FILING DATE: 2002-06-14
SPIOR FILING DATE: 2002-06-14
SPIOR OF SEQ ID NOS: 2699
TENNAMER OF SEQ ID NOS: 2699
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                                                                                                                                                                                                                                                                                                                                    Length 725;
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                                                                                                                                                                                                                                                                                                                                                                      le-65;
                                                                                                                                                                                                                                                                                                                                100.0%; Score 228; D
100.0%; Pred. No. 1e-
ive 0; Mismatches
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 17 LENGTH: 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 849, Application US/10342887; Publication No. US20040058340A1; GENERAL INFORMATION:
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243 GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT 302
GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGCAGTAGTGGGTT 180
                        243 GTGATCTTCAAGACCATTGTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT 302
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                                                                                                                                                                                                                                         Sequence 849, Application US/10172118

Publication No. US20000224374A1

GENERAL INFORMATION

APPLICANT: Dai, Hongive

APPLICANT: He, Yudong

APPLICANT: Mao, Mac

APPLICANT: Maisley, Peter

APPLICANT: Wanders, Chris

APPLICANT: Van de Vijver, Marc

APPLICANT: Wanders, Research Septer

APPLICANT: Wanders, Research Septer

APPLICANT: Wanders, Research Septer

APPLICANT: Wanders, Research Septer

APPLICANT: Wanders, Chris

APPLICANT: Wanders, Research Septer

APPLICANT: Wanders, Septer

TITLE OF INVENTION NUMBER: US/10/172,118

CURRENT FILING DATE: 2002-06-14

NUMBER OF SEQ ID NOS: 2699

SEQ ID NOS: 2699

TYPE: DNA

OGRANISM: Homo sapiens

PUBLICATION INPORMATION:

DATABASE BETRY DATE: 2001-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCCAAAGAAGCT
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                                                                                                                       303 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 1e-65;
Matches 228; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       303 CAGGATTCCATGGACCACAAGCAAACCCCAAAGCTCGAAGACT 350
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                                                                                           181 CAGGATTCCATGGACCACCTGGACAAGCAAACCCCAAACTCCGAAGACT 228
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US-10-170-385-396
US-10-170-385-396
Sequence 396, Application US/10170385
Publication No. US20030203372A1
GENERAL INPORMATION:
APPLICANT: Ward, Neil Raymond;
APPLICANT: Kan, On
APPLICANT: Man, On
APPLICANT: White, Jonathan
APPLICANT: Binley, Katie Mary
APPLICANT: Binley, Katie Mary
APPLICANT: Rayner, William Nigel
APPLICANT: Rayner, Stuart
APPLICANT: Kingsman, Susan Mary
                                                                                                                                                                                                                                    -10-172-118-849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 CAGCCAGATGCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGAGTGTCCCAAAGAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
US-10-641-643-1165
Sequence 1165, Application US/10641643
Sequence 1165, Application US/10641643
Publication No. US2004007700341
GENERAL INFORMATION:
Susan G. Stuart
Jeffrey J. Sellhamer
Jeffrey J. Sellhamer
GENE EXPRESSION
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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MEDIUM TYPE: Floppy disk
COMPUTER: BW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect, 6.1 for windows/MS-DOS G.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-AUG-2003
CLASSIFICATION: <URNown>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 CAGGATTCCATGGACCACCTGGACAAGCAAACCCCAAACTCCGAAGACT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 228; DB 13; Best Local Similarity 100.0%; Pred. No. 1e-65; Matches 228; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
APPLICANT: Krige, David
TILE OF INVENTION: ANALYSIS METHOD
FILE REFERENCE: 532682000100
CURRENT APPLICATION NUMBER: US/10/170,385
CURRENT FILING DATE: 2002-06-12
PRICR APPLICATION NUMBER: PCT/GB02/01662
PRICR APPLICATION NUMBER: PCT/GB01/05458
PRICR PILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 549
SOFTWARR: FastSEQ for Windows Version 4.0
SSOTUM NO 396
                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
CORGANISM: Homo Sapiens
US-10-170-385-396
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; ORGANISM: Homo sapiens
US-10-388-360-377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TCAGTGCAGAGGCTCGCGGAGCTATAGAAGAATCACCAGCAAGTGTCCCAAAGAAGCT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCCAAGCAGAAGTGGGTT 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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US-10-133-013-210

Sequence 210, Application US/10133013

Sequence 210, Application US/10133013

Sequence 210, Application US/10133013

Sequence 210, Application US/10133013

Sequence 210, Application US-10133013

APPLICANT: Bardoman, Olga

APPLICANT: Bandman, Olga

APPLICANT: Bandman, Olga

TITLE CF INVENTION: GENESA ASSOCIATED WITH VASCULAR DISEASE

FILE REFERENCE: PA-0049 US

CURRENT FILING DATE: 2002-04-25

PRIOR APPLICATION NUMBER: 60/287,067

PRIOR FILING DATE: 2001-04-27

NUMBER OF EGO ID NOS: 271

SOFTWARE: PERL PROGram

SEQ ID NO 2: 271

LENGTH: 756
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100.0%; Score 228; DB 15; Length 7
Best Local Similarity 100.0%; Pred. No. 1e-65;
Matches 228; Conservative 0; Mismatches 0; Indels
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OTHER INFORMATION: Incyte ID No. US20030166903A1 470784cB1
                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 228; DB 17; Best Local Similarity 100.0%; Pred. No. 1e-65; Matches 228; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                      CLONE: 9187434
SEQUENCE DESCRIPTION: SEQ ID NO: 1165 :
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1165:
SEQUENCE CHARACTERISTICS:
                                                                                           LENGTH: 741 base pairs
TYPE: nucleic acid
STRANDEDESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENEANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
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Sequence 377, Application US/10388360

Publication No. US2003022528A1

GENERAL INFORMATION:

APPLICANT: GENOMIC HEALTH

APPLICANT: Crohin, Maureen T.

APPLICANT: Shak, Steve

APPLICANT: Michael Graham

ITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES

TILE REFERENCE: 39740-0001US

CURRENT APPLICATION UNDER: US/10/388,360

CURRENT FILING DATE: 2003-09-18

PRIOR FILING DATE: 2002-09-18

PRIOR FILING DATE: 2002-09-18

PRIOR FILING DATE: 2002-03-13

NUMBER OF SEQ ID NOS: 384

SOCTWARE: FastSEQ for Windows Version 4.0

LENGTH: 757
262 GIGAICTICAAGACCAITGIGGCCAAGGAGAICIGIGCIGACCCCAAGCAGAAGIGGGTT 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTTATAACTTCACCAATAGGAAGATC 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCCAAAGAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GIGAICTICAAGACCATIGIGGCCAAGGAGATCIGIGCIGACCCCAAGCAGAAGTGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTTATAACTTCACCAATAGGAAGATC
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                                                              181 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 228
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                                                                                                                      322 caddatrccarddacaccrcdacaadcaaacccaaacrccaadacr 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 13; Length 757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 228; DB 13; Length '
Best Local Similarity 100.0%; Pred. No. 1e-65;
Matches 228; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: August 31, 2004, 09:18:28
Job time : 256 secs
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August 30, 2004, 16:49:12; Search time 1941 Seconds (without alignments) 4133.145 Million cell updates/sec
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228
1 cagocagatgcaatcaatgc.....aaacccaaactccgaagact 228
                                                                                                                                                                                                           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                 37577330 seqs, 17593059518 residues
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Maximum Match 100%
Listing first 45 summaries
                              - nucleic search, using sw model
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length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Gaps

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Result

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                                         TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT
                                                                                                                                  GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT
                                                                                                                                                                       121 GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCCAAGCAGAAGTGGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Koenegen, Frank
TITLE OF INVENTION: Higher molecular weight entities and uses therefor
FILE REPERENCE: 2385978
FILE REPERENCE: 2385978
CURRENT APPLICATION UNMBER: US/10/449,831A
CURRENT FILING DATE: 2003-05-30
PRIOR APPLICATION NUMBER: USSN 60/384878
PRIOR APPLICATION NUMBER: USSN 60/384878
NUMBER OF SEQ ID NOS: 237
SOFTWARE: PATE: 1002-05-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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0
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                                                                                                                                                                                                                                                                                                             181 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 228; DB 51; Length 294; 100.0%; Pred. No. 7.5e-58; ive 0; Mismatches 0; Indels 0
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; APPLICANT: Lukashev, Matvey
; TITLE OF INVENTION: Hematology/Immunology Array
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1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
181 CAGGATICCAIGGACCACTIGGACAAGCAAACICCGAAGGACT
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
US-09-221-481-519
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US-09-442-366A-1139
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                                                                                                                                                                                                                                                                                                                                                                                                 104 CASCCAGATGCATCAATGCCCCCAGTCACTGCTGTTATAACTTCACCAATAGGAAGATC 163
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Best Local Similarity 100.0%; Pred. No. 7.9e-58;
Matches 228; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 161, Application US/09442384B
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: LUKashev, Matvey
TITLE OF INVENTION: Hematology/Immunology Array
FILE REPERENCE: CLON-006C1P15
CURRENT APPLICATION NUMBER: US/09/442,384B
CURRENT FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: US/09/63,375
PRIOR APPLICATION NUMBER: US/09/63,375
PRIOR APPLICATION NUMBER: US/09/63,375
NUMBER OF SEQ ID NOS: 830
SOFTWARE: PastSEQ FOR Windows Version 4.0
SEQ ID NO 161
LENGTH: 348
    CURRENT APPLICATION NUMBER: US/09/442,384A
CURRENT FILING DATE: 1999-11-17
PRIOR PILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 830
SOFTWARE: PASTESEQ for Windows Version 4.0
SEQ ID NO 161
LENGTH: 348
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, OTHER INFORMATION: Nucleic Acid Probe. US-09-442-3848-161
                                                                                                                                                                                                                         ), OTHER INFORMATION: Nucleic Acid Probe. US-09-442-384A-161
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ORGANISM: Artificial Sequence
                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Seguence
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US-09-442-384B-161
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61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCCAAAGAAGCT 120 121 GIGAICTICAAGACCATIGIGGCCAAGGAGAICIGIGCIGACCCCAAGCAGAAGIGGGIT 180 223 104 CAGCCAGATGCAATGCCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC 163 124 GIGAICTICAAGACCATIGIGGCCAAGGAGAICIGIGGTGACCCCAAGCAGAAGIGGGTT 283 9 164 TCAGIGCAGAGGCTCGCGGAGCTATAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT 1 CAGCCAGATGCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC . 0 181 CAGGATTCCATGGACCACCTGGACAAGCAAACCCCAAACTCCGAAGACT 228 284 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 331 284 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 331 Length 349; Indels Query Match 100.0%; Score 228; DB 20; Best Local Similarity 100.0%; Pred. No. 7.9e-58; Matches 228; Conservative 0; Mismatches 0; Query Match 100.0%; Score 228; DB 16; Best Local Similarity 100.0%; Pred. No. 7.9e-58; Matches 228; Conservative 0; Mismatches 0; Sequence 1139 Application US/09442366A
Sequence 1139 Application US/09442366A
GENERAL INFORMATION
PAPPLICANT: Chenchik, Alex
APPLICANT: Lukashev, Matvey E.
TITLE OF INVENTION: Human Array
FILLE REPERENCE: CLON-006CIP13
CURRENT APPLICATION NUMBER: US/09/442,366A
CURRENT FILING DATE: 1998-03-11-7
PRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 2216
SEQ ID NO 1139
LENGTHRARE: FEATESQ for Windows Version 4.0
LENGTH: 349 US-09-221-481-519
US-09-221-481-519
Sequence 519, Application US/09221481
GENERAL INCRANTION:
FRIED CANT: Chenchik, Alex
APPLICANT: Chenchik, Matvey
TITLE OF INVENTION: Human Array
FILE REFERENCE: CLON-006CIP6
CURRENT APPLICATION NUMBER: US/09/221,481
CURRENT APPLICATION NUMBER: 09/053,375
PRIOR APPLICATION NUMBER: 09/053,375
PRIOR FILING DATE: 1998-12-28
FRIOR FILING DATE: 1998-03-31
NUMBER: OF SEQ ID NOS: 589
SEQ ID NO 519
LENGTH: 349
LENGTH: 349 ; OTHER INFORMATION: Synthetic gene fragment US-09-442-366A-1139

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100.0%; Score 228; DB 20; 100.0%; Pred. No. 7.9e-58;
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APPLICANT: Chenchik, Matvey
ITILE OF INVENTION: Human Cardiovascular Array
FILE REFERENCE: CLON-006CIP10
CURRENT APPLICATION NUMBER: US/09/442,589B
CURRENT FILING DATE: 1999-11.17
PRIOR APPLICATION NUMBER: 09/053,375
PRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 1194
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                          Mismatches
                                        TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: nucleic acid probe
US-09-442-589A-37
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Best Local Simi
Matches 228;
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       SEQ ID NO 37
LENGTH: 349
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LENGTH: 349
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                                                                                 GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT 180
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100.0%; Pred. No. 7.9e-58;
iive 0; Mismatches 0;
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TITLE OF INVENTION: Hematology/Immunology Array
FITLE OF INVENTION: Hematology/Immunology Array
FILE SEPERANCE: CLON-006CIP15
CURRENT APPLICATION NUMBER: US/09/442,384
CURRENT APPLICATION NUMBER: 09/053,375
PRIOR APPLICATION NUMBER: 09/053,375
PRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 415
SEQ ID NO 161
LENGTH: 349
TYPE: DNA
CRENISM: Artificial Sequence
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APPLICANT: Lukashev, Matvey
TITLE OP INVENTION: Human Cardicvascular Array
FILE REPERENCE: CLON-006CIP10
CURRENT APPLICATION NUMBER: 10509/442,589A
CURRENT FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 09/053,375
PRIOR FILING DATE: 1998-03-31
NUMBER OF SEQ ID NOS: 597
SOFTWARE: FastSEQ for Windows Version 4.0
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; OTHER INFORMATION: Nucleic Acid Probe.
US-09-442-384-161
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; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
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Best Local Similarity 100.
Matches 228; Conservative
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US-09-442-589A-37
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163 223 GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT 180 163 120 223 180 224 Grearcricaagaccarreregeccaagagarcrereregecceaageagagagarrere 283 GTGATCTTCAAGACCATTGTGTGTGTGTGTGTGTGTGACCCCAAGCAGAGTGGGTT 104 CAGCCAGATGCAATGCCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC 1 CAGCCAGATGCAATGCCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT 164 TCAGTGCAGAGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT 121 GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCCAAGCAGAAGTGGGTT 1 CAGCCAGATGCAATGCCCCAGTCACCTGCTGATAACTTCACCAATAGGAAGATC 104 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTTATAACTTCACCAATAGGAAGATC 61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT ; 0 Length 349; CAGGATTCCATGGACCACCTGGACAAGCAAACCCCAAACTCCGAAGACT 228 284 cadgarrccarddaccaccrcaacaagcaaacccaaacrcccaagacr 331 Query Match 100.0%; Score 228; DB 20; Length 349; Best Local Similarity 100.0%; Pred. No. 7.9e-58; Matches 228; Conservative 0; Mismatches 0; Indels 0 181 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 228 284 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 331 Indels

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TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT
                                                                                                 GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCCTGACCCCCAAGCAGAAGTGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Koenegen, Frank
TITLE OF INVENTION: Higher molecular weight entities and uses therefor
TITLE OF INVENTION: Higher molecular weight entities and uses therefor
TITLE OF INVENTION: Higher molecular weight entities and uses therefor
CURRENT APPLICATION NUMBER: US/10/449,831A
CURRENT FILING DATE: 2003-05-30
PRIOR PILING DATE: 2002-05-31
NUMBER OF SEQ ID NOS: 237
SOFTWARE: PATENTIN VERSION 3.2
SOFTWARE: Patentin Version 3.2
LENGTH: 405
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                                                                                                                                                                                                                                                                                                     298 caddarrccarddaccaccrddacaadcaaacccaaacrccaagacr 345
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US-09-287-618-16749
; Sequence 16749, Application US/09287618
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.;
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED;
; TITLE OF INVENTION: ROW VARIOUS CDNA LIBRARIES
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-768
; CURRENT PILLING DATE: 1999-04-02;
; UNMBER OF SEQ ID NOS: 35865
; SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                       181 CAGGALTCCATGGACCACCTGGACAAGCAAACCCCAAACTCCGAAGACT
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100.0%; Pred. No. 8.3e-58;
ive 0; Mismatches 0;
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OTHER INFORMATION: Human MCP-1 chimeric construct
                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 213, Application US/10449831A; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 228; Conservative
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; LOCATION: (1)..(399)
US-10-449-831A-213
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                   Sequence 1911, Application US/09534843

Sequence 2011, Application US/09534843

SEQUENCEAUT: Seilhamer, Jeffrey J. APPLICANT: Seilhamer, Angelo M. APPLICANT: Stuart, Susan G. APPLICANT: Stuart, Susan G. APPLICANT: Stuart, Susan G. APPLICANT: Maughton, Rebecca E. TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING SIGNAL TRANSDUCTION MOLEC TILE OF INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING SIGNAL TRANSDUCTION MOLEC CURRENT FILING DATE: 2000-03-24

CURRENT FILING DATE: 2000-03-24

CURRENT FILING DATE: 2000-03-24

NUMBER OF SEQ ID NOS: 49783

SOFTWARE: PERL PROGRAM

SEQ ID NOS: 49783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAAACTCCGAAGACT 228
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APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED; TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES; FILE REFERENCE: 20411-768; CURRENT APPLICATION NUMBER: US/09/287,618; CURRENT FILING DATE: 1999-04-02; SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 15642
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100.0%; Score 228; DB 17;
Best Local Similarity 100.0%; Pred. No. 8.3e-58;
Matches 228; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: hu01345546
US-09-534-843-7971
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LOCATION: (1)...(403)
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 100.
Matches 228; Conservative
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US-09-287-618-15642
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                                                                                                                               Length 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gearing, David P.
APPLICANT: Gearing, David P.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.2009-001
CURRENT APPLICATION NUMBER: US/09/726,791
CURRENT FILING DATE: 2000-11-30
PRIOR PRIOR APPLICATION NUMBER: 60/168,127
PRIOR PRIOR APPLICATION NUMBER: 60/168,127
PRIOR FILING DATE: 1999-11-30
NUMBER OF SEQ ID NOS: 1870
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 973
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Best Local Similarity 100.0%; Pred. No. 8.4e-58,
Matches 228; Conservative 0; Mismatches 0;
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; GENERAL INFORMATION:
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NAME/KEY: misc_feature
COCATION: (1)...(437)
OTHER INFORMATION: n = A,T,C or G
                                     TYPE: DNA
CRGANISM: Homo sapiens
US-09-287-618-16749
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ORGANISM: Homo sapiens
; SEQ ID NO 16749
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US-09-726-791-973
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APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Seilhamer, Angelo M.
APPLICANT: Seilhamer, Angelo M.
APPLICANT: Stuart, Suarn G.
APPLICANT: Stuart, Suarn G.
APPLICANT: Stuart, Suarn G.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
TITLE OP INVENTION: POLYNUCLEOTIDES ENCODING OR REGULATING SIGNAL TRANSDUCTION MOLECT URRENT APPLICATION NUMBER: US/09/534,843
CURRENT APPLICATION NUMBER: US/09/534,843
CURRENT FILING DATE: 2000-03-24
Prior application data removed - refer to PALM or file wrapper
SOFTWARE: PERL Program
SOFTWARE: PERL Program
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; OTHER INFORMATION: Incyte ID No: hu01000080
US-09-534-843-7953
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Job time : 1944 secs
Application US/09534843
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Best Local Similarity 100.
Matches 228; Conservative
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ORGANISM: Homo sapiens
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RESULT 1
AV661469
LOCATION
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                  August 30, 2004, 16:49:12; Search time 1465 Seconds (without alignments) 4647.493 Million cell updates/sec
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228
1 cagccagatgcaatcaatgc.....aaacccaaactccgaagact 228
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                               OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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2: em_esthum:*
3: em_esthum:*
5: em_estpol:*
6: em_estpol:*
7: em_estpol:*
10: gb_est2:*
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	_	AA047099 zk74a08.r	AV714555 AV714555	BX490080 DKFZp686B
		ΔI		497 9 AA047099	AV714555	BX490080
		DB		6	σ	13
	Query	Length	432 9	497	513	549
ф	Query			100.0	100.0	100.0
		Score		228	228	228
	Result	No.	1 1	2	m	4

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2 BM70491 2 BM70861 2 BM88825 3 BQ63144 AL697816	0 AW772 3 BU730 3 BO631 2 BM973 3 BU685 3 BU685	CB26796 BF33932 AV661137 CD68642 CD63883 CD64028	BF34381 4 CD64114 4 CD52344 4 CD64149 4 CD641069 4 CD640108	4 CD52242 AV716926 2 BQ00166 4 CA30738 4 CD64113 AV717442 3 BU19925	14 CD52018 9 AV733621 13 BQ224954 13 BU22217 14 CD522574 13 BU401003 10 BF211527
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ALIGNMENTS

	AV661469 432 bp mRNA linear EST 16-JAN-2002	ION AV661469 GLC Homo sapiens cDNA clone GLCGSG05 3', mRNA sequence.		AV661469.1 GI:9882483	S EST.	Homo sapiens (human)		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.			Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,	Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X.,	Hu, G., Gu, J., Chen, Z. and Han, Z.		by comparing gene expression profiles of hepatocellular carcinoma	with those of corresponding noncancerous liver			RD 11752456		Chinese National Human Genome Center at Shanghai	351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai	201203, P. R. China	Tel: 86-21-50801919(ex.45)
AV661469	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM			REFERENCE	AUTHORS				TITLE			JOURNAL	MEDLINE	PUBMED	COMMENT				

Not I

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Gaps

09

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Homo sapiens but herazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

E. (Saes I. t. 5313)

I. (Saes I. t. 5313)

Song, H., Gu, Y., Yang, Y., Gao, G., Xiao, H., Li, Y., Huang, Q., Zhou, J., Song, H., Gu, Y., Yang, Y., Gao, G., Xiao, H., Li, N., Qian, B., Gao, X., Lu, G., Cheng, Z., ad, M., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Cheng, Z., ad, M., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Cheng, Z., ad, Han, Z., Chones

Lu Unpublished (2000)

Contact: Zeguang Han

Chinese National Human Genome Center at Shanghai

Sol Guo Shouling Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai

Zoll 203, P. R. China

Tel: 86-21-5080199 (ex. 45)

Fax: 86-21-5080199 (ex. 45)

Fax: 86-21-5080199 (ex. 45)

Fax: Shanghai.

This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                            /dev stemmer adult"
/lab host="adult"
/lab host="DH10B"
/clone_lib="Soarse pregnant_uterus_NbHPU"
/note="Organ: uterus; Vector: pT7T3-Pac; Site_1: Not I;
Site_2: Eco RI; 1st strand cDNA was primed with a Not I oligo(dT) primer [5;
AACTGGAAGAATTCGCGGCCCTTTTTTTTTTTTTTTTT 3';
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by M. Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AV714555 DCB Homo sapiens cDNA clone DCBADG05 5', mRNA sequence. AV714555 LB GI:10796072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0, Mismatches
                                                                                                      /mol_type="mRNA"
db_xref="CDB:3803121"
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/clone="IMAGE:488534"
/sex="female"
                                                                                organism="Homo sapiens"
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        High quality sequence stop: 487.
                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 CAGCCAGATGCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCCAAAGAAGCT 120
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(Dases 1 to 497)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoes, Dietrich, N., DuBuque, T., Favello, A., Gish, W., Haukins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Trevaskis, E., Underwood, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R., and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                            /tissue_type="corresponding non cancerous liver tissue"/dev stage="Adult"
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/clone_lib="GLC"
/clone_lib="GLC"
/chore="Vector: pBluescript sk(-); Site_1: BcoRI; Site_2:
KhOT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 741 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 432;
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Fax: 86-21-50801922
Email: hanzagechgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
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100.0%; Pred. No. 1.1e-52;
iive 0; Mismatches 0;
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
                                                                                                                           /organism="Homo sapiens"
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/clone="GLCGSG05"
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Fax: 314 286 1810
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DKFZp686B1371 r1 686 (synonym: hlcc3) Homo sapiens cDNA clone

DKFZp686B1371 s', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKPZ); Emissive S. wiemann@dkfz- heidelberg.de;
sequenced by MediGenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. No s1 sequence
                                                                                                                                                                                                                                                                                                                                                           134 CAGCCAGATGCAATCAATGCCCCCAGTCACCTGCTTATAACTTCACCAATAGGAAGATC 193
                                                                                                                                                                                                                                                                                                                                                                                                            TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT 120
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Ottenwaelder, B., Obermaier, B., Deutschenbaur, S., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Pobo, G., Han, M. and Wiemann, S. EST (Ottenwaelder, B., Obermaier, B., Deutschenbaur, S., Mewes, H.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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cDNA-collection"
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/dev_stage="mature"
/lab_host="bross.8"
/note=locB"
/note="Type:"pTriplEx2; Site_1: sfilA; Site_2: sfilB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone (DKFZp686B1371) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                    1 CAGCCAGATGCAATGCCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                         194 TCAGTGCAGAGGCTCGCGAGCTATAGAATCACCACAGCAGCAGCAGCTACAGAAGCT
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                                                                                                                                                                                                                             Length 513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT
                                                                                                                                                                                                                 100.0%; Score 228; DB 9; Length 5
100.0%; Pred. No. 1.2e-52;
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/db_xref="taxon:9606"
/clone="DCBADG05"
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Homo sapiens
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Unpublished (2003)
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                                                                                                                                                                                                                                                                           228;
                                                                                                                                                                                                                               Query Match
Best Local S
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| organism="Homo sapiens" |
| wol_type="mRNA" |
| wol_tsuge="mrna" |
| wol_te="mrna" |
| wol_te="mrna" |
| wollied polylinker; Site 1: Ecom |
| wollied golylinker; Site 2: Not I;
| wollied golylinker; Site 3: Not I;
| wollied golylinker; Site 1: Ecom |
| wollied golylinker; Site 2: Not I;
| wollied golylinker; Site 3: Not I;
| wollied golylinker;
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UI-E-CII-agf-h-04-0-UI.rl UI-E-CI1 Homo sapiens cDNA clone
UI-E-CII-agf-h-04-0-UI.5', mRNA sequence.
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                   CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTTATAACTTCACCAATAGGAAGATC
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            Length 549;
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                                                                                                                     Indels
Query Match 100.0%; Score 228; DB 13; Best Local Similarity 100.0%; Pred. No. 1.2e-52; Matches 228; Conservative 0; Mismatches 0;
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Seg primer: M13 Reverse.
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adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Bye Institute (NEI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BM708613 588 bp mRNA linear BST 28-FEB-2002 UI-E-CII-afw-i-08-0-UI.rl UI-E-CII Homo sapiens cDNA clone UI-E-CII-afw-i-08-0-UI 5', mRNA sequence.
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Fax: 319 315 8250
Email: bento-soares@uicwa.edu
Tissue Procurement: Dr. Gregg Hageman cDNA Library Preparation: Dr. M. Bento Soares, Univeristy of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
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Bonaido, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 563;
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Coordinated Laboratory for Computational Genomics
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100.0%; Pred. No. 1.3e-52;
iive 0; Mismatches 0;
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/clone="UI-B-CII-afw-i-08-0-UI"
/tissue_type="RPE and Choroid"
/dev_tage="adult"
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97044477
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Matches 228; Conservative
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BM708613
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/clone_lib="UI-E-CII"

/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_l: EcoR I; Site_l: Not I; modified polylinker; Site_l: EcoR I; Site_l: Not I; modified polylinker; Site_l: EcoR I; Site_l: Not I; library concaining the following tissue(a): RPE and Choroid. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonuclectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BM888255 59-2002 S93 bp mRNA linear BST 08-MAR-2002 IMM174 Human Trabecular Meshwork cDNA library Homo sapiens cDNA 5',
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1 (bases 1 to 593)
Wirtz.M.K., Samples,J.R., Xu,H., Severson,T. and Acott,T.S.
Wirtz.M. Expression Profile and Genome Location of cDNA Clones from an Infant Human Trabecular Meshwork Library
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGCCAGATGCAATCAATGCCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
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Glaucoma Genetics Lab
Oregon Health Sciences University
3375 S.W. Terwilliger Blvd., Portland, OR 97201-4197, USA
Tel: 503-494-4698
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/mol_type="mRNA"
/db.xref="taxon:9606"
/tisque_type="eye"
/cell_type="trabecular meshwork"
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Email: wirtzm@ohsu.edu
Seg primer: T7 Reverse.
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A LOGACIA BROWN, J. Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wyle, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, B., Ronko, I., Bennett, J., Schmitt, A., Theising, B., McCann, R., Cole, R., Tasgareishvili, R., Williams, M., Jäckson, Y. and Bowers, Y.

Endocrine Pancreas Consortium
Unpublished (2000)
Cothact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BQ631442 117e04.yl HR85 islet Homo sapiens cDNa clone IMAGE:6030414 5' similar to SW:SY02_HUMAN P13500 SWALL INDUCIBLE CYTOKINE A2 PRECURSOR ;, mRNA sequence.
             /olone_lib="Human Trabecular Meshwork cDNA library"
/note="Vector: pcDNA3; Site 1: EcoRI; Site 2: EcoRI; Human
cdNA library made from mRNA isolated from Erabecular
meshwork calls established fom eyes from 6 individuals,
ages 2 weeks to 2 years. Cells were harvested at passages
3 through 6. Invitrogen made a unidirectional cDNA library
from the mRNA from the frozen cells using a pcDNA3 vector
and TPO10F'' host cells."
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Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 594)
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Pred. No. 1.3e-52;
; Mismatches 0; Indels 0;
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Location/Qualifiers
host="TOP10F'"
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100.0%; Pr
tive 0; 1
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BQ631442.1 GI:21682960
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                       228; Conservative
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Email: dmelton@bi
                                                                                                                                                                                                                                                                                            Similarity
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Best Local S
Matches 228
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/mol_type="mRNA"

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AL697816 616 bp mRNA linear EST 04-SEP-2003
DKFZp686E04104 r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKFZp68E04104 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
sequenced by MediGenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. No s1 sequence
available.
                                           /lab.host="DH10B"
/clone lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
Not1; Site_2: Nho1; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~lkb. 5'
Size-selected on agarose gel. Average insert size ~lkb. S'
Amplified one . Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@ingate.wustl.edu, Tel:
114-362-1916, Fax: 314-747-2692."
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1 (bases 1 to 616)
2 (bases 1, Obermaier, B., Mewes, W., Mewes, H.W., Weil, B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone (DKFZp686E04104) is available at the RZPD in Berlin. Plass contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de. Location/Qualifiers
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/olone="IMAGE:6030414"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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Unpublished (2001)
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Best Local Similarity
Matches 228; Conserv
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genne Sequencing Center
Clone distribution: NCT-CGAP clone distribution information can be
info@imaga-lini.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 465.
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                                                                                                                                                                                                                             134 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC 193
                                                                                                                                                                                                                                                                TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCCAAAGAAGCT 120
                                                                                                                                                                                                                                                                                               194 TCAGTGCAGAGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT 253
                                                                                                                                                                                                                                                                                                                                                           254 GTGATCTTCAAGACCATGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT 313
                                                                                                                                                                                             CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC 60
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NCI - CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP);
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="666 (synonym: hlcc3)"
/note="vector: pTriplEx2; Site_1: SfilA, Site_2: SfilB;
cDNA-collection"
                                                                                                                                                                                                                                                                                                                                      GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGGAGTGGGGTT
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Query Match

Best Local Similarity 100.0%; Pred. No. 1.3e-52;

Matches 228; Conservative 0; Mismatches 0; Indels
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AW772091.1 GI:7704153
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Unpublished (1997)
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University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 5242, USA
7e1: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
sequence: 1-39, AAT.rich#Low_complexity (matched compliment)
Seq primer: M13 FORWARD
POLYA=Yes.
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                                                                                                                                                                                                                                                                                                                                                                                                          61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT 120
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Bukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi,

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 628)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                     503 CAGCCAGATGCAATCAATGCCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
                                                                                                                                                                                                                                                                                1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
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(cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "
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                                                                                                                                                             Length 623;
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Genome Res. 6 (9), 791-806 (1996)
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/organism="Homo sapiens"
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BU730951.1 GI:23655357
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modified polylinker; Site_1: ECOR I; Site_2: Not I; UT-E-CII is a normalized CDNA library containing the following tissue(s): RPE and Choroid. The library was following tissue(s): RPE and Choroid. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pTTTJ-pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)B tail. The sequence tag for this library is ACCTA. (This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute TAG TISSUE=RPE and Choroid TAG LIB=UI-E-CII TAG SEQ=ACCTA" (NEI)

ORIGIN

ö 1 CAGCCAGATGCAATGCCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC 60 Gaps ö Length 628; Indels 0 Score 228; DB 13; Pred. No. 1.3e-52; 0; Mismatches 100.0%; Matches 228; Conservative Similarity Query Match Best Local S

563 503 121 GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT 180 502 grgarcricaagaccarreregeccaaggagarcrereregecceaagcagaagreegr 443 61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCCAAAGAAGCT 442 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 395 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 228 181 임 임 ò ò g ò

RESULT 12 BQ631169/c

634 bp mRNA linear EST 02-JUL-2002 similar to SW:SY02 HUMAN P13500 SMALL INDUCIBLE CYTOKINE A2 PRECURSOR; , mRNA Sequence. LOCUS

BQ631169.1 GI:21682687 ACCESSION

Homo sapiens (human) Homo sapiens ORGANISM VERSION KEYWORDS SOURCE

Bukaryota; Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 634) REFERENCE

AUTHORS

TITLE JOURNAL COMMENT

Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Lahiller, L., Marran, M., Page, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Milliams, T., Jackson, Y. and Bowers, Y. Bendocrine Pancreas Consortium
Unpublished (2000)

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium Harvard University, Howard Hughes Medical Institute Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, rel: 617-495-1812 Fax: 617-495-8557 MA 02138

Email: dmelton@biohp.harvard.edu Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on

/USB TITES THE NOTE OF THE NOT contact: Dr. Hiroshi Inoue /organism="Homo sapiens" obtaining a clone please contact (himoue@im.wustl.edu)
Seq primer: -40UP from Gibco
High quality sequence stop: 439. .634 source FEATURES

ORIGIN

ö 180 607 CAGCCAGAIGCAAICAAIGCACCCAGICACCIGCIGIIAIAACIICACCAAIAGGAAGAIC 548 120 487 GIGATCTICAAGACCATTGIGGCCAAGGAGATCIGIGCIGACCCCAAGCAGAAGIGGGTI 428 9 121 GTGATCTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTT 61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAAGTGTCCCCAAAGAAGCT 1 CAGCCAGATGCAATCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC Gaps .; 0 181 CAGGATTCCATGGACCAGCTGGACAAGCAAACCCAAACTCCGAAGACT 228 CAGGATICCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 380 Length 634; Indels 100.0%; Score 228; DB 13; Similarity 100.0%; Pred. No. 1.3e-52; 88; Conservative 0; Mismatches 0; Local Simi hes 228; Query Match Matches 셤 δ 셤 ò g $\stackrel{>}{\circ}$ 8

BM973445/c RESULT 13

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EST 20-FEB-2003 BM973445 UI-CF-EC1-abx-n-09-0-UI.s1 UI-CF-EC1 Homo sapiens CDNA clone UI-CF-EC1-abx-n-09-0-UI 3', mRNA sequence. BM973445.1 GI:19591036 LOCUS DEFINITION ACCESSION VERSION

Homo sapiens (human) Homo sapiens KEYWORDS SOURCE ORGANISM

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I, Dases I to 640. Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene discovery REFERENCE AUTHORS TITLE

Genome Res. 6 (9), 791-806 (1996) Contact: McCray, PB 97044477 8889548 MEDLINE PUBMED COMMENT JOURNAL

McCray Lab

University of Iowa 2014 University of Iowa Med Labs, Iowa City, IA 52242, USA 2014 University of Iowa Med Labs, Iowa City, IA 52242, USA Tel: 319 356 7171
East: 319 356 7171
East: Bardl.mccrayoulowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

FEATURES

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438 CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 391
                                                                                                                                                                 Genome Res. 6 (9), 791-806 (1996)
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                       (bases 1 to 640)
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//wol type="memory saplems"
//wor stage="hadut and Fetal"
//lab host="PulluB (Life Technologies) (Tl phage resistant)"
//lab host="PulluB (Life Technologies) (Tl phage resistant)"
//lone lib="Ul-CF-ECI"
//worest Lung / Wector: pT773-Pac (Pharmacia) with a modified polylinker; Site 1: Ecok I; Site 2: Not I;
//wore="Organ: Lung; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site 1: Ecok I; Site 2: Not I;
//worestructed according to Bonaldo, Lennon and Soares,
//work 19 and week 42. The library was constructed according to Bonaldo, Lennon and Soares,
//work 19 and week 42. The library was constructed according to Bonaldo, Lennon and Soares,
//work 19 and Library tag sequence that is located between the Not I site and the AAGTGCTTAC.
//www.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modity.com.modit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BU685364 innear EST 07-OCT-2002
UI-CF-DU1-aav-j-23-0-UI.S2 UI-CF-DU1 Homo sapiens cDNA clone
UI-CF-DU1-aav-j-23-0-UI 3', mRNA sequence.
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).

The following repetitive elements were found in this cDNA Seq prime: 1.36, AT Tich#Low_complexity (matched compliment) POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              619 CAGCCAGATGCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATG 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGTCCCAAAGAAGCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       499 Grearcricaagaccarrerescoaagagarcrererescoccaaggagagagaggerr 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CAGCCAGATGCAATGCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGGATTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACT 228
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                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAG_LIB=UI-CF-EC1
TAG_SEQ=AAGTGCTTAC"
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and_380-383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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KEYWORDS
SOURCE
ORGANISM
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BU685364/c
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ORIGIN

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ACCESSION

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/ Organisms... mouncy sagirems // Mol types many sagirems // Lissue types many Lung Epithelial Cells... // Lissue types many Lung Epithelial Cells... // Lab _/ Lost= many lung; Vector: pr773-pec (Pharmacia) with a modified polylinker; Site_1: Econ I; Site_2: Not I; UI-CF-DUI is a normalized CDNA library containing the following tissue(s): Primary Lung Epithelial Cells The library was constructed according to Bonaldo. Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an oligo-dT primer containing a Not I site Double stranded CDNA was ligated to an Econ I adaptor, digested with Not I, and cloned directionally into pf73-Pac vector. The oligomucleotide used to prime the synthesis of first-strand contains a library tag sequence that is located between the Not I site and the Not II site sequence tag for this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: paul-mccray@ulowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.openbiosystems.com) or from Open Biosystems
(www.openbiosystems.com).
The following repetitive elements were found in this cDNA
Seq primer: Mi3 FORWARD
POLYA=Yes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
1 (bases 1 to 640)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 GTGATCTTCAAGACCATTGTGGCCCAAGGAGATCTGTGCTGACCCCCAAGCAGAAGTGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CAGCCAGATGCAATCAATGCCCCCAGTCACCTGCTGTTATAACTTCACCAATAGGAAGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          558 TCAGTGCAGAGGCTCGCGAGCTATAGAAGAATCACCAGCAGCAAGTGCCCCAAAGAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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TAG_LIB=UI-CF-DUI
TAG_SEQ=GGCTGTAGGC"
                                                                                                                                                                                                                                                                                                                                              University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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/dev_stage="Adult"
/dev_stage="Adult"
/dev_stage="Adult"
/lab host="PHIOB (Life Technologies)"
/clone lib="NoI CGAP Chi"
/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
/noI G CAP Chi is a cDNA library containing the following
tissue(s): Chondrosarcoma Grade II The library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Orthoapedics conthoars br. M. Bento Soares, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soarescaniowa.edu
The following repetitive elements were found in this cDNA sequence: 1-39, AT rich#Low_complexity (matched compliment) POLYA=Yes.
                                           BQS73817 644 bp mRNA linear EST 19-JUN-2002 UI-H-EZO-bax-c-19-0-UI.S1 NCI_CGAP_Ch1 Homo sapiens cDNA clone UI-H-EZO-bax-c-19-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      503
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                                                                                                                                                                                                                                                 Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 644)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
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TAG_LIB=UI-H-EZ0
TAG_SEQ=ATCTAATATG"
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ilarity 100.0%; Pred. No. 1.3e-52;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mkNa"
/mol_type="mkNa"
/clone="UI-H-EZ0-bax-c-19-0-UI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                        BQ573817.1 GI:21477134
                                                                                                                                                                                                            Homo sapiens (human)
Homo sapiens
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Best Local Similarity
Matches 228; Conserv
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                                                   LOCUS
DEFINITION
RESULT 15
BQ573817/c
                                                                                                                           ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
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Search completed: August 31, 2004, 03:47:21 Job time : 1473 secs Lipis Page Blank (uspto)